OM protein - protein search, using sw model

March 13, 2006, 18:52:59; Search time 75.2941 Seconds (without alignments) 58.355 Million cell updates/sec Run on:

US-09-529-206E-15 Perfect score:

1 TVSGNILTIR 10 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* Database

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

		Description	Aav05980 Human can	Himan	Human			Aae07727 Human NY	Human 5	Human	Human	0 Human	1 Human	Aau01544 HLA-DR53				Adx08648 Class II	Aae07742 Human ESO	Adil9891 Human HLA	Adil9048 Human HLA	Peptic	-	_	Add71521 HLA-DP4 b	_
SUMMARIES		ΩI	AAY05980	AAY05988	AAE07788	AAE07728	AAE07726	AAE07727	AAE07786	AAE07787	AAY52440	AAB69940	AAB69944	AAU01544	AAU01540	AAE07769	ADW50855	ADX08648	AAE07742	ADI19891	AD119048	ADJ58397	ADZ67819	AAE07718	ADD71521	ADZ67810
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AAE07717	AAU85110	ABG79131	ADG89697	ADQ10452	ADS80932	ADK68648	ADK68657	ADQ10455	ADS80935	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164	AAU01535	AAE07714	AAU84818
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25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127. AAY05980 standard; peptide; 10 AA. (first entry) 16-AUG-1999 AAY05980; RESULT 1

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lolon cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidhey cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine.

Homo sapiens.

WO9918206-A2.

15-APR-1999.

98WO-US019609 21-SEP-1998;

97US-0061428P. 08-OCT-1997;

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Wang RF, Rosenberg SA;

WPI; 1999-277270/23.

Cancer antigen NY ESO1/CAG-3.

Claim 17; Page 64; 88pp; English.

This sequence represents cancer peptide ESO10-127 that corresponds to amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAV05965), a new and potent tumour antigen capable of aliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAV05966), portions of them and their squainst cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of

prostate, ovarian, pancreatic and thyroid cancers

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This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see AAX58599) 30 Epitopes (see AAY0588-Y06017) were identified. The present peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAX05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
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cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HiA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, luckacmia, uterine cancer, lore carvical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                     100.0%; Score 47; DB 2; Length 10; 100.0%; Pred. No. 0.004;
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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1 The MHC-II epitopes from the cancer antigen, NY ESO-1 and human leucocyte crown YESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR or HLA-DR or HLA-DR or HLA-DR or HLA-DR or Experisor of the gene are promising candidates for restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection of attained mandor CD8+ T cell response squainst any given the generation of antibody and/or CD8+ T rell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope recognised
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                                                                                                                                                                                                                                                                                                                                                                                    Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.
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                                                                                                         Gaps
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                                                                  100.0%; Score 47; DB 2; Length 10; 100.0%; Pred. No. 0.004;
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29-SEP-2000; 2000US-0237107P.
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Sequence 14 AA;

Human NY ESO-1 MHC class II restricted T cell epitope #12.

(first entry)

06-NOV-2001

AAE07726;

AAE07726 standard; peptide; 15 AA.

AAE0772 RESULT

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by aliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection of antibody and/or CD8+ T cell responses against any given target antigen and/or CD8+ T cell responses against any given target antigen and/or happen and to induce tumour-specific humoralments and antigen and to induce tumour-specific humoralments and antigen and tell protects and protect and protect and protect and protect and protect and concer. The present sequence is MHC class II restricted T cell epitope of human NY ESO-1 protein
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                                                  Gaps
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100.0%; Score 47; DB 4; Length 14; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                AAE07728 standard; peptide; 14 AA.
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29-SEP-2000; 2000US-0237107P.
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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitopes) darived from the cancer antigen, NY ESO-1. The MHC-II epitopes (C from NY ESO-1 are recognised by CD4+T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for HLA-DP restricted. The products of the gene are promising candidates for HLA-DP restricted. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection of energy the product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+T cell responses against any given the generation and contact the presence of cancer.
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                                                                                                                                   Human; major histocompatibility complex; MHC; vaccine; metastasis;
class II restricted T cell epitope, MHC-II epitope; cancer antigen;
NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
tumour-specific humoral-mediated immunity; cancer; cytostatic;
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29-SEP-2000; 2000US-0237107P.
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100.0%; Score 47; DB 4; Length 14; 100.0%; Pred. No. 0.0061; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 10; Conservative

1 TVSGNILTIR 10

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Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.

(first entry)

06-NOV-2001

Human, major histocompatibility complex; WHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR crestricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention. treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of calls expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-
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                                                                                                                                                                                 Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
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                                                                                                                                           Human NY ESO-1 MHC class II restricted T cell epitope #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                       AAE07727 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 16; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Marches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JAN-2001; 2001WO-US002765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protection from metastasis.
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-496851/54.
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                                                                                                                                                                                                                                                                                                                                                  WO200155393-A2
                                                                                                                                                                                                                                                                    immunotherapy
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
                                                               AAE07727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang R,
NAE07727
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New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as

Example 6; Fig 6A; 134pp; English.

protection from metastasis.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

28-JAN-2000; 2000US-0179004P. 29-SEP-2000; 2000US-0237107P. 26-JAN-2001; 2001WO-US002765

WO200155393-A2.

02-AUG-2001

immunotherapy Homo sapiens ΰ

Rosenberg SA,

Wang R,

WPI; 2001-496851/54.

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II captored from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR crastricted. The products of the gene are promising candidates for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral.

CE peptide used in the characterisation of the NY ESO-1 epitope recognised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 47; DB 4; Length 15; 100.0%; Pred. No. 0.0067; 2. No. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE07787 standard; peptide; 15 AA.
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Gaps

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AAE07786 standard; peptide; 15 AA.

RESULT 7

AAE07786;

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TVSGNILTIR 10

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TVSGNILTIR

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The invention relates to the identification and isolation of major histocompatibility (MHG) class II restricted T cell epitope (MHG-II epitope) derived from the cancer antigen, NV ESO-I. The MHG-II epitopes from NV ESO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The preducts of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection of the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral mediated immunity against cancer. The present sequence is human NY ESO-I epitope recognised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer; tumour; antigen; MHC; major histocompatility complex; Class II; T-cell; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; overian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restrated T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4 T lymphocyte; human leuccoyte antigen; tumour-specific humoral-mediated immunity; cancer; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour antigen NY-ESO-1 peptide #13.
                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Fig 6A; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                    Zeng G;
                                                                                                                                                                                                                                          26-JAN-2001; 2001WO-US002765.
                                                                                                                                                                                                                                                                                  28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protection from metastasis.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                               immunotherapy
                                                                                                                         Homo sapiens
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Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.

Claim 4; Page 22; 49pp; English.

Old LJ;

Alexander K,

Scanlan M,

Chen Y,

Jager E,

Stockert E, Jager Gure A, Ritter G;

WPI; 2000-038483/03.

(LUDW-) LUDWIG INST CANCER RES

98US-00165546.

99WO-US006875. 98US-00062422

24-MAR-1999; 17-APR-1998; 02-OCT-1998;

28-OCT-1999

Homo sapiens WO9953938-A1

Synthetic.

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tumour antigen, NY-ESO-1 (AAYS2430) which can bind to MHC(major historompatibility Class II HIA-DRS3 molecules, thereby stimulating proliferation of helper T-cells. CDNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer CDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal covary and testis but not in normal colon, kidney, liver, brain, cesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lumg cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lumg cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells
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HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity
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Query Match
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                                                                                                                                                                              The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small
                                                                                                          Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                     Scanlan M;
                                                                                                                                                                                                                                                                                                                           100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                     Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen Y,
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                    Old LJ, Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NY-ESO-1 HLA-DR53 binding motif #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knuth A,
                                                                                                                                                                                                                                                                                     lung carcinoma or bladder carcinoma
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(SLOK ) SLOAN KETTERING INST CANCER RES
                                        CANCER RES
                                                                                                                                                            Example 16; Page 27; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB69944 standard; peptide; 18 AA.
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                            LUDW-) LUDWIG INST CANCER RES
                                       SLOK ) SLOAN KETTERING INST C
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(CORR ) CORNELL RES FOUND INC.
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          99US-00359503
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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                                                                    Stockert E,
                                                                                       WPI; 2001-182822/18.
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                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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                                                                                                                                           patient.
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Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; muman leukocyte antigen-determining region; disease progression; disease cegression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a human NY-ESO-1 tumour rejection antigen precursor fragment which recognises and binds to HIA-DRE3. WY-ESO-1 and SGX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MRC) Class II molecules such as human leukocyte antigen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-DR53 recognising NY-ESO-1 peptide #6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Page 19; 62pp; English.
                                                                                                                                                                                                                            English.
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                                                                                                                                                                                                                            20pp;
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10s 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive bubject in order to stimulate the helper T cells. An MHC class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoractive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the
             $$$$$$$$$$$$$$$$$$$$$
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Sequence 18 AA;

ö Gaps ; 0 100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084; 0; Indels 0; Mismatches 10; Conservative Local Similarity Query Match Matches

ò 셤 RESULT 13

AAU01540 standard; peptide; 18 AA (first entry) 18-JUL-2001 AAU01540;

HLA-DR53 recognising NY-ESO-1 peptide #2.

NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; human leukocyte antigen-determining region; disease progression; disease regression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.

Homo sapiens.

WO200123560-A2

26-SEP-2000; 2000WO-US026411.

99US-00408036 29-SEP-1999; (LUDW-) LUDWIG INST CANCER RES.

Pfreundschuh M; WPI; 2001-266156/27. Tureci O,

Sahin U,

leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells. Polypeptides binding to major histocompatibility complex class II human

Example 13; Page 19; 62pp; English.

The sequence represents a human NY-ESO-1 tumour rejection antigen precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigendetermining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in

free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoractive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the

888888888888888

Sequence 18 AA;

Gaps ö 100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084; ive 0; Mismatches 0; Indels Local Similarity 100. Les 10, Conservative Query Match Matches

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16 1 TVSGNILTIR 10 TVSGNILTIR

ò 셤 RESULT

AAE07769

AAE07769 standard; peptide; 18 AA.

AAE07769;

(first entry) 06-NOV-2001 Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy

Homo sapiens.

WO200155393-A2.

02-AUG-2001.

26-JAN-2001; 2001WO-US002765.

28-JAN-2000; 2000US-0179004P. 29-SEP-2000; 2000US-0237107P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Wang R, Rosenberg SA,

WPI; 2001-496851/54.

New NY-ESO cancer peptide or MHC class II restricted ${\tt T}$ cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.

Claim 84; Page 84; 134pp; English.

The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NV ESO-I. The MHC-II epitopes from NV ESO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a manmal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-I gene product. The cancer peptides are also

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The invention describes an isolated NY-ESO-1 peptide (I), consisting of amino acids 80-109, 87-98, 108-119, 121-132 or 143-154 of a sequence of 180 (SI) amino acids Fully defined in the specification. Also described are: a composition (II) useful in stimulating a CD4 + T cell response, comprising (I) and an adjuvant; a composition (III) useful in stimulating a T cell response in a subject, comprising (I) and at least one additional peptide; an isolated nucleic acid molecule (IV) consisting of a nucleotide sequence which encodes a peptide, where the amino acid sequence is chosen from 80-109, 87-98, 108-119, 121-132 or 143-154 of 180 (C (S1); an expression vector (V) comprising (IV) operably linked to a promoter; a recombinant cell (VI) comprising (IV) a recombinant cell (VII) comprising (IV); a recombinant cell (VII) comprising (IV) and an isolated CD4 + T cell (VIII) which class II molecule. (I) is useful for treating cancer. This is the amino conditions acid sequence of a NY-ESO-1 peptide.
                                                                                                                                                                                         ö
useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 HLA DR restricted T cell cancer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; immune stimulation; cancer; cytostatic; neoplasm; NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel NY-ESO-1 peptide that binds to human leukocyte antigen class II molecules, useful for treating cancer.
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100.0%; Score 47; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                 100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084;
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                                                                                                                                                                                                                                                                                                                                                   ADW50855 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2003; 2003US-0474893P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gnjatic S, Atanackovic D,
                                                                                                                              Query Match
Best Local Similarity 100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NY-ESO-1 peptide 121-138
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                                                                                                               Sequence 18 AA;
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Search completed: March 13, 2006, 19:03:56 Job time: 77.2941 secs

us-09-529-206e-15.rpr

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Page

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds (without alignments) 80.975 Million cell updates/sec

US-09-529-206E-15 1 TVSGNILTIR 10 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result		Query				
No.	Score	Match	Length	DB	ΩI	Description
-	36	76.6		7	T13099	major tail protein
7	36	9.9/		~	AD2753	υ
m	36		3	7	B97534	
4	35	74.5	335	7	A89837	hypothetical prote
D.	34	72.3	-	ч	RSBSOF	
9	34	72.3		~	T41234	translation initia
7	34	72.3		N	AB3218	2-hydroxyacid dehy
6 0	34	72.3		0	G86835	hypothetical prote
6	34	72.3	1266	~	A85989	
10	34	72.3		~	F91143	
11	33	70.2	14	٦	TPBPP1	н
12	33	70.2		~	S18683	gene R protein - E
13	33	70.2	411	α	G95241	MATE efflux family
14	33	70.2		~	B98106	hypothetical prote
15	33	70.2		~	F85253	hypothetical prote
16	33	70.2	4	~	B81033	N-acetylglutamate
17	33	70.2	4	7	A81977	probable amino-aci
18	33	70.2	449	7	802011	serotonin receptor
19	33	70.2	4	~	A43956	serotonin receptor
20	33	70.2	471	N	S11280	serotonin receptor
21	33	70.2		7	S40689	5-hydroxytryptamin
22	33	70.2		~	A34863	serotonin receptor
23	33	70.2		~	E96674	hypothetical prote
24	33	70.2	918	~	T02759	
25	33	70.2	-	~	F71405	
56	32	68.1	102	7	C86898	hypothetical prote
27	32	68.1	N	~	B81972	O)
28	32	68.1	. 135	~	D81029	conserved hypothet
59	32	68.1	187	N	137105	5-HT2c receptor -

hypothetical prote	hypothetical prote	probable oxidoredu	lysozyme (EC 3.2.1	hypothetical prote	conserved domain p	conserved hypothet	uncharacterized pr	S-adenosylhomocyst	hypothetical prote	sigma 1 protein pr	serotonin receptor	serotonin receptor	serotonin receptor	serotonin receptor	alkylhalidase homo
H75390	S57550	C87158	525234	A69325	G95146	E98014	C97059	E70401	865162	HMXRS3	JS0616	A43951	A32605	S23562	T30590
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234	245	289	316	344	347	347	376	418	451	455	458	459	460	479	491
68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1
	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
32															

ALIGNMENTS

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Major tail protein V - phage N15
NiAlternate names: protein gp13
C;Species: phage N15
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accesion: T13099
C;Accesion: T13099
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K. submitted to the EMBL Data Library, May 1998
R;Accession: T13099
A;Retence number: Z17603
A;Accession: T13099
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-245 - HEN>
A;Residues: 1-245 - HEN>
A;Caross-references: UNIPROT:064327; UNIPARC:UPI000009BA91; EMBL:AF064539; NID:g3192683; C;Genetics:
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Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  A;Note: gene 13
C;Superfamily: phage lambda major tail protein V
                                                                                                                                                                                                                                                                                                                                                                                                                                         76.6%;
77.8%;
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Les 7; Conservative
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Best Local S:
Matches 7
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209 TVSGNTLTV 217

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lipoic Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AD2753
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, 's erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2.317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Acession: AD2753
A,Accession: AD2753
A,Status: preliminary

A;Molecule type: DNA A;Residues: 1-323 <KUR> A;Cross-references: UNIPROT:Q8UFG1; UNIPARC:UP100012E6BE; GB:AE008688; PIDN:AAL42442.1 A;Experimental source: strain C58 (Dupont)

C'Genetics:
A;Gene: 11ps
A;Map position: circular chromosome
C;Superfamily: 11poyl synthase

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ribosomal protein L6 - Bacillus stearothermophilus
N.Alternate names: ribosomal protein BL10
C;Species: Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Accession: A02766; B39085; S59061
R;Kimura, M.; Rawlings, N.; Appelt, K.
FEBS Lett. 136, 58-64, 1981
A;Title: The amino acid sequence of protein BL10 from the 50S subunit of the Bacillus st
A;Accession: A02766
A;Accession: A02766
A;Accession: A02766
                                                                                                                                                                                                                                                                        A; Residues: 1-177 < KIM>
A; Cross-references: UNIPARC: UPI0000050F95

B; Archieller Gerchman, S.E.
J. Biol. Chem. 266, 880-885, 1991

A; Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from Ba A; Reference number: A39085; MUID:91093287; PMID:1985969

A; Accession: B39085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-244 <LYN>
A;Residues: 1-244 <LYN>
A;Cross-references: UNIPROT:094476; UNIPARC:UPI000012D3B6; EMBL:AL035075; PIDN:CAA22640
A;Cross-references: strain 972h-; cosmid c1919
C;Genetics:
A;Gene: SPDB:SPCC1919.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 8-170 cRAM>
A; Cross-references: UNIPARC:UP10000173A98; GB:MS7622
A; Cross-references: UNIPARC:UP10000173A98; GB:MS7622
B; Urlaub, H.; Kruft, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.
EMBO J. 14, 4578-4588, 1995
A; Title: Protein-RNA binding features and their structural and functional implications
A; Reference number: S59051; MUID:96003638; PMID:7556101
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24;
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A,Molecule type: DNA
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Pred. No. 34;
2; Mismatches
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Pred. No. 24;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Superfamily: ribosomal protein L6/L9
C, Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 149-163 <URL>
A;Cross-references: UNIPARC:UP10000173A99
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55.6%;
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141 TVAGNVLT 148
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A; Introns: 12/2; 36/2
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C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: A89837
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Reference number: A89758; MulD:21311952; PMID:11418146
A; Recession: A89837
A; Status: preliminary
A; Residues: 1-335 KURS
A; Residues: 1-335 KURS
A; Cross-references: UNIPROT:Q99VV7; UNIPARC:UPI0000549A2; GB:BA000018; PID:g13700555; F
A; Experimental source: strain N315
C; Genetics: A60619
C; Superfamily: probable sodium-dependent phosphate transporter MTH1885
                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: B97534
R; Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: B97534
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Redidues: 1-232 <KUR>
A; Cross-references: UNIPROT: Q8UFG1; UNIPARC: UPI000012E6BE; GB: AE007869; PIDN: AAK87227.1;

    Agrobacterium tumefacie

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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004
C;Accession: B97534
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                                         Score 36; DB 2
Pred. No. 18;
1; Mismatches
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Pred. No. 18;
1; Mismatches
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A,Map position: circular chromosome
C,Superfamily: lipoyl synthase
                                               76.6%;
70.0%;
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                            Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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189 TVPGNYLTVR 198
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189 TVPGNYLTVR 198
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hypothetical protein EC84118 [imported] - Escherichia coli (strain O157:H7, substrain R C;Species: Escherichia coli (5.5pecies: Escherichia coli 2004 (5.5pace: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 (5.5pacession: F91143 (5.5pace
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A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI0000D082E; GB:BA000007; PIDN:BAB37541.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                           A,Molecule type: DNA
A,Residues: 1-1266 <STO>
A,Residues: 1-1266 <STO>
A,Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI0000D082E; GB:AE005174; NID:g12517869;
A,Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A,Gene: Z4604
C;Superfamily: Escherichia coli hypothetical protein yhdp
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2; Length 1266;
Pred. No. 1.9e+02;
2; Mismatches 1; Indels
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C,Superfamily: phage Pl tail fiber protein R
C,Keywords: tail fiber
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66.7%;
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Best Local Similarity 66.77
Matches 6; Conservative
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Matches 6; Conservative
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1017 TISGNTLTL 1025
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A;Status: preliminary
A;Molecule type: DNA
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2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004 C;Accession: AB318 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Rage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 S. Alathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Ress. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Recession: G86835
A;Status: preliminary
A;Residues: 1-314 <STO>
A;Residues: 1-
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A.Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Superfamily: 2-hydroxyacid dehydrogenase
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ISGNILTL 100
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-311 < KUR>
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A;Molecule type: DNA
A;Residues: 1-144 <GUI>
A;Cresidues: 1-16tences: UNIPROT:P22946; UNIPARC:UPI0000138778; GB:M25470; NID:g341349; PIDN
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                    tail Tiber protein R - phage P1
C;Species: phage P1
C;Species: phage P1
C;Accession: JS0460
R;Guidolin, A.; Zingg, J.M.; Arber, W.
Gene 76, 239-243, 1989
A;Title: Organization of the bacteriophage P1 tail-fibre operon.
A;Reference number: P80109; WID:89326122; PMID:2526777
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A;Gene: EC94118
C;Superfamily: Bscherichia coli hypothetical protein yhdP
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A, Gene: MATE transporter
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Generic Becherichia coli plasmid p15B
C; Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
R; Sandmeier, H; Iida, S.; Huebner, P; Hiestand-Nauer, R.; Arber, W.
Nyacheric anumber: 318680; MUD: 92051368; PMID: 1945872
A; Recession: 518683
A; Status: translation not shown
A; Residues: 1-144 < SAN>
A; Cross-references: UNIPROT: Q47426; UNIPARC: UPI00000B4972; EMBL: X62121; NID: 942224; PIDN
C; Generics:
A; Generics:
A; Generics:
A; Generics: Plasmid
C; Superfamily: phage P1 tail fiber protein R
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: 695241
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95241
A;Residues: Dreliminary
A;Molecule type: DNA
A;Residues: 1-411 *KUR>
A;Cross-references: UNIPROT:097NG5; UNIPARC:UPI000051ADC; GB:AE005672; PIDN:AAK76128.1;
A;Genetics: SP2065
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Pred. No. 31;
2; Mismatches
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A,Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <KOR>
A;Cross-references: UNIPROT:Q8DN77; UNIPARC:UPI00000E3724; GB:AE007317; PIDN:AAL00679.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein A74922170 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C.Accession: F85253
R.anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir Nature 402, 769-777, 1999
A.Aritle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A.Reference number: A85001; MUID:20083488; PMID:10617198
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Abd.ccule type: DNA
A,Residues: 1-428 <STO>
A,Cross-references: UNIPROT:Q9SUG4; UNIPARC:UPI00000A1769; GB:NC_001268; NID:g7269062; i
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Pred. No. 98;
3; Mismatches
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C,Superfamily: F-box containing protein
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EMBL; AJ003149; CAA05908.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
MUN; HGNC:2491; CTAGIB.
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(c) 1993 - 2006 Biocceleration Ltd
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDILINE=99289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen B., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
                                 05x554
05zvd1
05lnu4
05lea1
09pt82
09pt83
06irp9
06nx22
08t4d0
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Q93fv1
               QSWWD6_LEGPL
QSXVD1_LEGPH
TOLB_STLPO
GSILEA1 BACFN
Q9PT83_XENLA
Q9PT83_XENLA
Q6PT83_XENLA
Q6NX22_XENTR
Q6NX22_XENTR
Q6NX20_DROME
Q9VSQ0_DROME
Q9DRGQ_DROME
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15-DEC-1998 (Rel. 37, Last seq.
10-MAY-2005 (Rel. 47, Last anno
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set of germ line— and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
                                                                                                                                                                                                                     *10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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MEDLINE-21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557; Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Beposito T., Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M., Nelson D.L.;
                                                          100.0%; Score 47; DB 1; Length 180; 100.0%; Pred. No. 0.55;
                                                                                   Indels
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Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                       Gly-rich.; B122C5C2C8BE1569 CRC64;
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                                                                                    0; Mismatches
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Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
Homo sapiens (Human).
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17992 MW;
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Q7LBY4;
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Best Local Similarity 100...
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Antigen; Transmembrane
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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"Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on matrobial commensalism.";
Nucleic Acids Res. 32:4937-4944(2004).
-!- SIMILARITY: Belongs to the small heat shock protein (HSP20)
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100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.55;
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Pred. No. 11;
                                                                               Indels
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Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR.2000) to the EMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
NON TER
SEQUENCE 1 1
SEQUENCE 142 AA; 13895 WW; 27EBE922AC4ACC7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP006840; BAD39931.1; -; Genomic_DNA.
GO; GO:0006457; P:protein folding; IEA.
GO; GO:0006986; P:response to unfolded protein; IEA.
InterPro; IRR002068; Hsp20.
PROSITE; PS01031; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
COMplete Proteome; Heat shock.
SEQUENCE 141 AA; 15725 MW; C7BABABCFC50FD36 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=T / IAM 14863;
PubMed=15383646; DOI=10.1093/nar/gkh830;
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01-0cT-2000 (TrEMBLrel. 15, Last sequenc)
01-0cT-2002 (TrEMBLrel. 22, Last annotat
Hypothetical protein LAGE-2 (Fragment).
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25-OCT-2004 (TrEMBLrel. 28, Last
25-OCT-2004 (TrEMBLrel. 28, Last
HSp20 family heat shock protein.
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Q9NY13;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q67QW2_SYMTH_PRELIMINARY;
Q67QW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=STH946;
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                                                                               10; Conservative
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Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              STRAINECE3;
MEDLINE-97286510; PubMed-9141657; DOI=10.1016/S0378-1097(97)00069-4;
Tate R., Riccio A., Iaccarino M., Patriarca E.J.; (lipoic acid "Cloning and transcriptional analysis of the lipA (lipoic acid synthetase) gene from Rhizobium etli.";
FEMS Microbiol. Lett. 149:165-172(1997)
-!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur atoms into an octanoyl group bound to acyl carrier protein (ACP)
-!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur atoms into an octanoyl group (By similarity).
-!- CATALYTIC ACTIVITY: Octanoyl- [acyl-carrier protein] + 2 sulfurs =
                                                                                                                                                                   LIPA_RHIET STANDARD; PRT; 322 AA.
005941;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
11-JUL-1998 (Rel. 48, Last annotation update)
11-JUL-1998 (Rel. 48, Last annotation update)
11-JUL-1999 (Rel. 48, Last annotation protein lipha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipoyl-[acyl-carrier protein].
-!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and an exchangeable S-adenosyl-L-methionine (By similarity).
-!- COFACTOR: Binds 1 3Fe-4S cluster (Potential).
-!- PATHWAY: Lipoate blosynthesis; sulfur-insertion step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases family. Lipa subfamily.
                                     Gaps
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Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
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Iron-sulfur 1 (3Fe-48) (Potential)
Iron-sulfur 1 (3Fe-48) (Potential)
Iron-sulfur 2 (4Fe-48-S-AdoMet) (Bimilarity).
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       2; Length 142;
                                    Indels
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InterPro; IPR006638; Blp3/MiaB/NifB.
InterPro; IPR003698; Lipoate synth.
InterPro; IPR003699; Lipoate synth.
InterPro; PTR10949; Lipoate synth; 1.
Pfam; PF04055; Radical_SAM; 1.
PIRSF; PIRSF005963; Lipoyl_synth; 1.
SMART; SM00729; Blp3; 1.
TIGRFAMS; TIGR00510; lipa; 1.
3Fe-48; 4Fe-48; Iron; Iron-sulfur; Metal-binding; Tra
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DB 7
                                  1; Mismatches
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      Score 39;
Pred. No.
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    83.0%;
88.9%;
                                  8; Conservative
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NCBI_TaxID=29449;
                                                                                         101 TVSGNILTM 109
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                                                             1 TVSGNILTI 9
   Query Match
Best Local Similarity
Matches 8; Conserv
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72
87
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Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L., Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F., Etlenne J., Glaser P., Buchrises C.;
"Evidence in the Legionella pneumophila genome for exploitation of host cell functions and high genome plasticity.";
Nat. Genet. 36:1165-1173(2004).
EMBL; CR628336; CAH12569.1; -; Genomic_DNA.
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Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrell B.G.;
"The chromosome 1 sequence of Theileria annulata.";
Submitted (APR-2005) to the RNBL/GenBank/DbBJ databases.
EMBL; CR940347; CA173760.1; -; Garcomic DNA.
SEQUENCE 617 AA; 67272 MW; 2A3696230D209B70 CRC64;
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                                                                                                                                                                                                                                                                                                        OrderedLocusNāmes=lpp1418;
Legionella pneumophila (strain Paris).
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
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Pred. No. 63;
2; Mismatches 0; Indels
Score 38; DB 1; Length 322;
Pred. No. 61;
2; Mismatches 1; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Theileria parva Tpr-related protein, putative.
ORFNames=TA21390;
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 80.9%;
70.0%;
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77.8%;
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Q5X5A2_LEGPA PRELIMINARY;
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Q4UGM9;
Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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188 TVAGNYLTVR 197
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                                                                                                                                                                                                                                                                                             Hypothetical protein.
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NUCLEOTIDE SEQUENCE
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InterPro; IPR011698; GATase_3.
Pfam; PR07685; GATase_3; 1.
Complete proteome.
SEQUENCE 250 AA; 27653 MW;
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Best Local Similarity
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PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
Ogata H., Renesto P., Audic Z., Nobert C., Blanc G., Fournier P.-E., Parinello H., Claverie J.-M., Raoult D.;
The genome sequence of Rickettsia felis identifies the first putative conjugative plasmid in an obligate intracellular parasite.";
PLOS Biol. 3:E248-E248(2009).
EMBL; CP000053; AAY61019.1; -; Genomic_DNA.
InterPro; IRR007460; DUF497.
Pfam; PF04365; DUF497.
SEQUENCE 94 AA; 11378 MW; D62F3CIDE3CF686E CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
BMBL, AE014295, AAN24266.1; -; Genomic_DNA.
GO, GO:0003824; F:catalytic_activity; IEA.
GO, GO:0009236; P:cobalamin biosynthesis; IEA.
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MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales; Bifidobacteriacea; Bifidobacterium.
NCBL TaxID=216816;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
14) SeptendiocusNames-RP 0168;
15 Crecteia felia (Rickettsia azadi).
16 Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
17 Rickettsiaceae; Rickettsieae; Rickettsiales;
                         Score 38; DB 2; Length 617;
Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.7%; Score 37; DB 2; Length 94; 77.8%; Pred. No. 28;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                          94 AA.
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                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possible cobyric acid synthase CobQ. OrderedLocusNames=BL0429;
                                                                                                                                                                                                                                                                        PRT;
                           80.9%;
  Ouery Match
Best Local Similarity 70.v.
Triconservative
Triconservative
                                                                                                                                                                                                                                                                      Q4UN39 RICFE PRELIMINARY;
Q4UN39;
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Matches 7; Conservative
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451 TISGNTLTIK 460
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                                                                                                                1 TVSGNILTIR 10
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56 VDGNILTVR 64
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Nuclection of S., Rushiok C., Vandenesch F., Kunst F.,

Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

Richit M., Jarraud S., Buchitser C.,

Reienne J., Glaser P., Buchitser C.,

Trichit M., Jarraud S., Buchitser C.,

Reienne J., Glaser P., Buchitser C.,

Thost cell functions and high genome plasticity.";

Nat. Genet. 36:1165-1173 (2004).

Nat. Genet. 36:1165-1173 (2004).

Rejolists, Iphl566;

Rejolists, Iphl566;

Rejolists, Iphl566;

Rejolists, Iphl566;

Rejolists, Iphl661;

Rejolists, I
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
26-0CT-2004 (TrEMBLrel 28, Last annotation update)
27-0CT-2004 (TrEMBLrel 28, Last annotation update)
28-0CT-2004 (TrEMBLrel 28, Last annotation update)
29-0CT-2004 (TrEMBL
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Legionella proemophila (strain Lens).
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
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Legionellaceae, Legionella.
NCBI_TaxID=272624;
                                                                                                                              Length 250;
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PROSITE; PS01136; UPF04; 1.
Complete proteome: Hypochetical protein.
SEQUENCE 330 AA; 37311 MW; BEF836DAP152E15E CRC64;
250 AA; 27653 MW; 7577954A609689CF CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                     78.7%; Score 37; DB 2;
87.5%; Pred. No. 75;
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QSWW87 LEGPL PRELIMINARY;
OSWW87;
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                                                                                                                                                                                                     Local Similarity 87.5 es 7; Conservative
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318 AA; 34113 MW; 0A0B7165033B6FCF CRC64;
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EMBL; AE015817; AAN56819:1; -; Genomic_DNA.
TIGR; SO3842; -.
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                                                                                                                                                         Name=gene 13;
                                                              RESULT 13
O64327 BPN15
ID O64327 RE
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Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M., Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J., Steahenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R., Pampou S., Georghiou A., Chou I.-C., Iannuccilli W., Ulz M.E., Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G., Ju J., Kalachikov S., Shuman H.A., Russo J.J.; "The genomic sequence of the accidental pathogen Legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
"The diploid Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                Length 334;
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Transmembrane.
SEQUENCE 1217 AA; 135897 MW; 1F2788D13CAD6DEC CRC64;
                                                                                                       EMBL; AE017354; AAU27544.1; -; Genomic_DNA.
EMBL; AE0120166; F:PAD binding; IEA.
EQ; GO:0016033; F:ENA processing; IEA.
InterPro; IPR001269; Du_synth.
EMBL; PE01207; Dus; 1.
ENGSITE; PS01136; UPF0034; 1.
COMPILE; PS01136; UFF0034; 1.
ENGSITE; PS01136; UFF0034; 1.
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Last annotation update)
                                                                                                                                                                                                                              78.7%; Score 37; DB 2; 66.7%; Pred. No. 1e+02; tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    OSAFO7_CANAL PRELIMINARY;
QSAFQ7;
                                                                                                                                                                                                                                        Local Similarity 66.7
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                                                                                                                                                                                                                                                                                             208 TINGNILTV 216
                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
ORFNames=CaO19.7011;
                                                                                                                                                                                                                                                                          1 TVSGNILTI 9
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Matches 6; Conserv
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Q5AFQ7 CAN
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CSTRAIN=NR-1;

MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

MEDLINE=22297686; PubMed=11.T., Nelson N.E., Methe B.A.,

MEDLINE=1.T., Paulsen I.T., Nelson N.E., Delson M.J.,

METHE D.H., Edonay J.F., Maduy R., Peterson J.D., Umayam L.A.,

MITCO, Wolf A.M., Vamathevan J.J., Weidman J.P., Impraim M.,

MITCO, Wolf A.M., Vamathevan J.J., Weidman J.P., Impraim M.,

MITCO, Wolf A.M., Paulsen C.M., Khouri H.M., Gill J.,

MITCABACK T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,

A Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,

MANNER J.C., Nealson K.H., Praser C.M.;

"Genome sequence of the dissimilatory metal ion-reducing bacterium

Shewanella oneidensis.";
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                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage N15.
Viruses; daDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
N15-like viruses.
NCBI_TaxID=40631;
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella.
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Smirnov I.K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF064539; AAC19050.1; -; Genomic_DNA.
PIR; T13099; T13099.
PIR; T13099; B102.2.
PFam; PF02368; B102.2.
SMART; SM06635; B102.2: 1.
SEQUENCE 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SO3842.
OrderedLocusNames=SO3842;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                         PRT;
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064327;
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636 TIAGNILTV 644
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                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last unotation update)
13-SEP-2005 (Rel. 48, Last unotation update)
14-SEP-2005 (Rel. 48, Last L.) (Lipoic acid synthase) (Lipoate synthase)
(Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase)
(Lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).

MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipoyl-[acyl-carrier protein]
--- CORACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and an exchangeable S-adenosyl-L-methionine (By similarity).
--- COFACTOR: Binds 1 3Fe-4S cluster (Potential).
--- PATHWAY: Lipoate biosynthesis; sulfur-insertion step.
--- SUBCELLUIAR LOCATION: Cytoplasmic (Potential).
--- SIMILARITY: Belongs to the biotin and lipoic acid synthetases family. LipA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDIINE=21608560; PubMed=11743193; DOI=10.1126/science.1066804;
MOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Mood D.W., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chan Y., Paulsen J.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                               Gaps
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Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizoblaceae; Agrobacterium.
                     76.6%; Score 36; DB 2; Length 318; 87.5%; Pred. No. 1.5e+02;
                                                             0; Indels
                                                                                                                                                                                                                                                323 AA
                                                             1; Mismatches
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
Query Match
Best Local Similarity 87...
7, Conservative
                                                                                                                                                                                                                                                STANDARD;
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153 TVSGNIIT 160
                                                                                                      1 TVSGNILT 8
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                                                                                                                                                                                                                                                LIPA AGRT5
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EMBL; AE009104; AAL42442.1; -; Genomic_DNA. EMBL; AE008069; AAK87227.1; -; Genomic_DNA.

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HAWARY ME 00206; -; 1.

HAWARY ME 00206; -; 1.

InterPro; IPR003689; Lipoate synth.

InterPro; IPR003689; Lipoate synth.

InterPro; IPR003197; Radical_SAM.

PANTHER, PTHR10949; Lipoate_Synth, 1.

Pfam; PF04055; Radical_SAM; 1.

Pirns; PTRSP005963; Lipoyl_synth; 1.

PIRSF; PIRSP00329; Blp3; 1.

TIGRREAMS; TIGR00510; lipA; 1.

TIGREAMS; TIGR00510; lipA; 1.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                               Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
similarity).
Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
similarity).
                                                                                                                                                                    Iron-sulfur 1 (3Fe-4S) (Potential).
Iron-sulfur 1 (3Fe-4S) (Potential).
Iron-sulfur 1 (3Fe-4S) (Potential).
Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By similarity).
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0
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Pred. No. 1.5e+02;
.; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                         74B294773BC784D2 CRC64;
                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 13, 2006, 19:14:21
Job time : 75.5882 secs
                                                                                                                                                                                                                                                                                            323 AA; 36341 MW;
                                                                                                                                                                                                                                                                                                                     76.68;
                                                                                                                                                                                                                                                                                                                                   70.0%;
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nes 7; Conservative
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66
72
87
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RESULT 1
US-09-359-503-9
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Sequence 125, App
Sequence 120, App
Sequence 120, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 58027, A
Sequence 42707, A
Sequence 2739, Ap
Sequence 329, App
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, Appl
Appli
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Sequence 8, Appli
Sequence 8, Appli
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Sequence 2614, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             March 13, 2006, 19:14:49; Search time 18.5882 Seconds (without alignments) 44.477 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       /cgm2_6/prodata/1/taa/5_COMB.pep:*
/cgm2_6/prodata/1/taa/6_COMB.pep:*
/cgm2_6/prodata/1/taa/H_COMB.pep:*
/cgm2_6/prodata/1/taa/PCTUS_COMB.pep:*
/cgm2_6/prodata/1/taa/RE_COMB.pep:*
/cgm2_6/prodata/1/taa/RE_COMB.pep:*
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-09-134-001C-5428
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S-09-270-767-58027
S-09-270-767-42707
S-10-104-047-2739
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5-09-833-039A-125
5-09-833-039A-120
5-09-833-039A-120
5-09-8341-825A-7
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US-09-408-036B-8
US-09-408-036B-12
US-08-791-495-9
US-08-791-798-8
US-09-751-798-8
US-09-392-714-25
US-09-341-829A-9
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-118-270-329
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                                                                                                                                                                                                                                      572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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ALIGNMENTS

to NY

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APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CT
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 47; DB 2; Length 18; 100.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/062,422

FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/337,263

FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182

FILING DATE: October 3, 1996
ATTORNEY/AGRY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-165-546D-13
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                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jagér, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                         100.0%; Score 47; DB 2; Length 18; 100.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                   0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: July 23, 1999
CLASSIFICATION ON THE STATE OF THE STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: HARBOR, NO. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09/359,503
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09359503 Patent No. 6251603
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TELEFAX: (212) 752-5958
INFORMATION FOR SEC ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
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; TOPOLOGY:
US-09-359-503-9
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US-09-359-503-13
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Sequence 12, Application US/09408036B

Sequence 12, Application US/09408036B

Sequence 12, Application US/09408036B

GENERAL INFORMATION:

APPLICANT: Tured, O31em

APPLICANT: Tured, O31em

APPLICANT: Tured, O31em

APPLICANT: Pfreundschuh, Michael

TITLE OF INVENTION: 1801ated Peptides Which Bind to MHC Class II Molecules and Uses

TITLE OF INVENTION: 1992-09-29

CURRENT APPLICATION NUMBER: US/09/408, 036B

CURRENT APPLICATION NUMBER: 09/344, 040

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 38

SEQ ID NO 12

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L0461/7005
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
7 TVSGNILTIR 16
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 600 A
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-408-036B-12
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CURRENT APPLICATION NUMBER: US/09/408,036B
CURRENT APPLICATION NUMBER: 09/344,040
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 47; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 6723832man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 318-3000
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Patent No. 6800730
GENERAL INFORMATION:
APPLICANT: Turici, Ozlem
APPLICANT: Salni, Ugur
APPLICANT: Pfreundschuh, Michael
                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Best Local Similarity 100.
Matches 10; Conservative
            STATE: New York
COUNTRY: USA
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127 TVSGNILTIR 136
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                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-751-798-8
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Yao-Tseng, Scanlan, Matthew,
APPLICANT: Chen, Yao-Tseng, Scanlan, Matthew,
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth, Drijfunt, Jan W.
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 66 Fifth Avenue
CITY: New York City
                                                                                                                                            Gaps
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                                                                                                 Score 47; DB 1; Length 180;
Pred. No. 0.16;
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                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; PENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM
COMPUTER: IBM
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08937263B
Patent No. 6274145
                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 318-3000
TELEPAX: (212) 752-5958
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 TVSGNILTIR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-937-263B-8
                                                                                                                                                                                                                                                                                                   US-08-937-263B-8
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THILD OF INVENTION: Antibodies Which Bind to NV-ESO-1 Cencer 1717E OF INVENTION: Antibodies Which Bind to NV-ESO-1 Cencer 1717E OF INVENTION: Associated Proteins. User Therefor, 1717E OF INVENTION: Truncated Proteins. User Therefore, 1717E OF INVENTION: Truncated Proteins. User Therefore, 1717E OF INVENTION: Ending Peptides Delived Therefore, 1717E New York City Proteins. User Therefore, 1717E New York City Williamson, New York City Williamson
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APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determi
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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0
                                       APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE NEPRERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT PILING DATE: 1999-10-18
CURRENT PILING DATE: 1999-10-18
FRIOR APPLICATION NUMBER: PCT/US/98/01445
NUMBER OF SEQ ID NUMBER: PCT/US/98/01445
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.16;
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APPLICANT: Stackert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849, 602
CURRENT FILING DATE: 2001-05-04
NUMBER: PATENTIN version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 125, Application US/09344040C
Partent No. 6548064;
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 30, Application US/09849602; Patent No. 6794501; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-344-040C-125
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION S30
PRIOR APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/917,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.16; cive 0; Mismatches 0; Indels
                                                                       DB 2; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, No. 6723832man D. REGISTRATION NUMBERS: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
                                                                  Query Match 100.0%; Score 47; DB 2; Length 18
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CIIY: New York City
STATE: New York
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SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 318-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 180 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                            127 TVSGNILTIR 136
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; ORGANISM: Homo sapiens
US-09-392-714-25
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                                                                                                                                                                                                                                                                                                        US-09-165-546D-15
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US-09-341-829A-9
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Fatent No. 6673350

GREAL INFORMATION

APPLICANT: Tureci, Ozlem

APPLICANT: Sahin, Ugur

APPLICANT: Preci, Ozlem

APPLICANT: Preci, Ozlem

APPLICANT: Prevandschuh, Michael

TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1

CURRENT APPLICATION NUMBER: US/09/833,039A

CURRENT APPLICATION NUMBER: US 09/409,455

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 131

SOFTWARE: PatentIn version 3.2

LENGTH. 0
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                                                                                                                                                                                                                                                                                                                  Query Match 89.4%; Score 42; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: LUD 5556.1

CURRENT APPLICATION NUMBER: US/09/344,040C

CURRENT FILING DATE: 1999-06-25

FRIOR APPLICATION NUMBER: US 09/105,839

PRIOR FILING DATE: 1998-06-26

PRIOR PILING DATE: 1998-06-26

FRIOR FILING DATE: 1997-05-05

NUMBER OF EQ ID NOS: 132

LENGTH: 9
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-344-040C-125
                                                                                                                                                                                                                                                                                                                                                                                                    CRGANISM: Homo sapiens US-09-833-039A-125
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US-09-833-039A-125
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Search completed: March 13, 2006, 19:18:49 Job time : 18.5882 secs

11, Appl 15, Appl 74, Appl 11, Appl 97, Appli 770, Ap 7, Appli 3, Appli 3, Appli 5024, Ap

Sequence Sequence Sequence Sequence

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Sequence:

Run on:

Searched:

Database

Result No.

Sequence Sequence Sequence

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; Sequence 15. Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, K-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL WHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 5; Length 14; 100.0%; Pred. No. 0.028; Live 0; Mismatches 0; Indels
US-10-117-937-74
US-10-295-027-386
US-10-296-027-386
US-10-188-832-139
US-10-777-053-11
US-10-777-053-11
US-10-837-217-11
US-10-837-217-11
US-10-837-217-11
US-10-87-217-13
US-10-87-217-13
US-10-87-217-13
US-10-185-523-3
US-10-182-506A-3
US-11-067-064-74
US-11-067-064-74
US-11-067-064-74
US-11-067-064-74
US-01-184-912-27
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-10-182-506A-17
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Best Local Similarity 100.
Matches 10; Conservative
         1 TVSGNILTIR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                              March 13, 2006, 19:51:56 ; Search time 60.4706 Seconds (without alignments) 69.096 Million cell updates/sec
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Sequence 3,
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Sequence 2
Sequence 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-182-506A-15

US-10-182-506A-16

US-10-751-088-13

US-10-851-884-8

US-10-851-884-12

US-10-851-884-12

US-10-164-121A-35

US-10-164-121A-35

US-10-164-121A-35

US-10-182-506A-65

US-10-941-150A-35

US-10-941-150A-35

US-10-941-150A-36

US-10-941-1404

US-10-182-506A-6

US-10-182-502-202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-182-8
US-10-207-655-71
US-10-026-066-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1867569 segs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                        US-09-529-206E-15
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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Gaps

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APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.037;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                               ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/662,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/97,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/09/25,182
FILING DATE: COCTOBER: US/07/25,182
FILING DATE: COCTOBER: US/07/25,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
       USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 13, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
                                                                                                  STREET: 666 Fifth Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 318-3400 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                   NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-751-088-13
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Gure, All, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, R-F
APPLICANT: Rosenberg, S A
APPLICANT: Rosenberg, S A
APPLICANT: Rosenberg, S A
APPLICANT: Rosenberg, S A
APPLICANT: Zeng, G
APPLICANT: APPLICANT: Rosenberg, S A
APPLICANT: APPLICANTON NOVEL MHC CLASS II RESTRICTED T CELL BPITOPES FROM THE CANCER
TITLE OF INVENTION: ANTIGEN, NY ESO-1
FILE REFERENCE: 217955
CURRENT APPLICATION NUMBER: US/10/182,506A
PRIOR APPLICATION NUMBER: PCT/US01/02765
PRIOR APPLICATION NUMBER: 60/179,004
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 5; Length 15; 100.0%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION WUMBER: PCT/USO1/02765
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR PLICATION NUMBER: 60/237,107
PRIOR PLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/10182506A Publication No. US20050136402A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 15
                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Matches 10; Conservative
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US-10-182-506A-16
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US-10-751-088-9
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WS-10-182-506A-65

Sequence 65, Application US/10182506A

Publication No. US20050136402A1

Sequence 65, Application US/10182506A

Publicant: Wang, R-F

APPLICANT: Wang, R-F

APPLICANT: Rosenberg, S A

APPLICANT: Zeng, G

TITLE OF INVENTION: ANTIGEN, NY ESO-1

FILE REFERENCE: 217955

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: PCT/US01/02765

PRIOR PRILICATION NUMBER: 60/179,004

PRIOR APPLICATION NUMBER: 60/179,004

PRIOR APPLICATION NUMBER: 60/237,107

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28
                                                                                                                                 APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Ffreundschuh, Michael
TITLE NEFENENCE: LUD 5624
CURRENT APPLICATION NUMBER: US/10/851,884
CURRENT APPLICATION NUMBER: US/09/408,036
PRIOR APPLICATION NUMBER: US/09/408,036
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 38
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                     ; Sequence 12, Application US/10851884; Publication No. US20040214284A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-10-851-884-12
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| Publication No. US20040214284A1
| GENERAL INFORMATION | US20040214284A1
| GENERAL INFORMATION | US20040214284A1
| APPLICANT: Tureci, Ozlem | APPLICANT: Sahin, Ugur | APPLICANT: Pfreundschuh, Michael | TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses 7 | TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses 7 | CURRENT FILING DATE: 2004-05-21 | PRIOR PAPLICATION NUMBER: US/09/408,036 | PRIOR PILING DATE: 1999-09-29 | PRIOR PILING DATE: 1999-06-25 | PRIOR PILING DATE: 1999-06-25 | PRIOR PILING DATE: 1999-06-25 | PRIOR PILING DATE: 1998-10-02 | PRIOR PILING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 anino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/ARMINES
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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RESULT 9 US-10-164-121A-35

RESULT 7

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Sequence 83. Application US/10491891
Fublication No. US20050059107A1
GENERAL INFORMATION:
APPLICANT: MAILLERE, BERNARD
APPLICANT: GASTELLI, FLORENCE
APPLICANT: GASTELLI, FLORENCE
APPLICANT: GEORGES, BERTRAND
ITILE OF INVENTION: WATHOOD OS SELECTING HLA-DP4 LIGANDS AND THE APPLICATIONS THEREOF
FILE REFERENCE: 25185801800xPCT
CURRENT APPLICATION NUMBER: US/10/491,891
CURRENT FILING DATE: 2004-04-15
FRIOR FILING DATE: 2002-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: VAN DER BRUGGEN, Pierre
APPLICANT: SOND-FALLEUR, Thierry
APPLICANT: BRECKPOT, Karine
APPLICANT: THIELEMANS, Kris
TITLE OF INVENTION: ISOLATED PEPTIDE WHICH BINDS TO HLA-CW*07 AND USES THEREOF
FILE REPERENCE: LUD-5853-US (10411307)
CURRENT APPLICATION NUMBER: US/10/941,150A
CURRENT FILING DATE: 2004-09-15
RIOR PEPTION NUMBER: US 60/504,874
PRIOR FILING DATE: 2003-09-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE PATENTION OF 33.2
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US-10-941-150A-35
          PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/179,004
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: 20
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                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic US-10-182-506A-38
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 20
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Faguence 34, Application US/10164078A

GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT:
APPLICANTON WINBER:
APPLICANT:
APPLICANT:
APPLICANTON WINBER:
AP
Sequence 35, Application US/10164121A
Publication No. US20030228308A1
APPLICANT: APPLICANT: Zhang, Yi
APPLICANT: APPLICANT: APPLICANT: APPLICANT: Traversari, Catra
APPLICANT: Traversari, Catra
APPLICANT: Traversari, Catra
TITLE OF INVENTION: 1801ated Peptides Which Bind to HLA-Cw6 Molecules And Uses Therefulls REFERENCE: LUD-5771
CURRENT APPLICATION NUMBER: US/10/164,121A
CURRENT PILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 36
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Publication No. US20050136402A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosenberg, S A
APPLICANT: Zeng, G
TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
TITLE OF INVENTION: AATIGEN, NY BSO-1
FILE REFERENCE: 217955
CURRENT FILLING NUMBER: US/10/182,506A
CURRENT FILLING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/02765
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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Matches 10; Conservative
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LENGTH: 20
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Search completed: March 13, 2006, 20:02:26 Job time : 61.4706 secs
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; Bequence 7, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 217955
CURRENT FILING DATE: 2002-10-28
FRIOR APPLICATION NUMBER: BCT/US01/02765
FRIOR APPLICATION NUMBER: 60/179,004
FRIOR APPLICATION NUMBER: 60/179,004
FRIOR PILING DATE: 2000-01-28
FRIOR PELING DATE: 2000-01-28
FRIOR PELING DATE: 2000-01-28
FRIOR PELING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 25
LENGTH: 25
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Publication No. US20050136402A1
GENERAL INFORMATION:
APPLICANT: Wang, R-F
APPLICANT: Rosenberg, S A
APPLICANT: Zeng, G
APPLICANT: Zeng, G
TITLE OF INVENTION: ANTIGEN, NY ESO-1
FILE REPERENCE: 217955
CURRENT APPLICATION NUMBER: US/10/182,506A
CURRENT FILING DATE: 2002-10-28
FRIOR APPLICATION NUMBER: PCT/US01/02765
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; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-491-891-83
PRIOR APPLICATION NUMBER: FR01/13352
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.2
SEQ ID NO 83
LENGTH: 25
                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-182-506A-6
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100.0%; Score 47; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/179,004
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE, PATENTIN VETBION 3.1
SEQ ID NO 6
                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Synthetic
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Sequence 36, Appl
Sequence 7, Appli
Sequence 412, Appl
Sequence 10549, A
Sequence 2739, Ap
Sequence 2739, Ap
Sequence 1556, Ap
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                                                                           March 13, 2006, 19:54:06; Search time 6.82353 Seconds (without alignments) 40.793 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USOF NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO3 NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO3 NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO3 NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO1 NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO1.NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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47, Appl
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            US-10-08-517-412
US-11-08-68-10549
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US-11-190-188-7
US-10-467-657-1556
US-10-995-561-901
US-10-995-561-901
US-10-645-788A-711
US-10-641-678-47
US-10-641-678-47
US-10-641-678-45
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US-11-052-554A-174
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US-10-641-678-70
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Sequence Sequence Sequence

US-11-129-741-2370 US-11-087-099-342 US-09-810-501-21 US-09-978-360A-516

Sequence

41, Appl 11290, A 43, Appl 55, Appl 155, Appl 183, Ap 183, Ap 183, Ap 183, Ap 183, Ap 183, Appl 193, Appl 193, Appl 194, Appl 1054, Appl 1056,	6776, Ap 265, App
Sequence Seq	Sequence
US-10-511-538-41 US-11-129-143-43 US-11-129-143-43 US-11-129-143-43 US-11-129-143-55 US-11-129-143-55 US-11-129-143-55 US-11-129-143-55 US-11-129-143-55 US-11-129-130 US-11-127-877-54 US-11-127-877-54 US-11-127-877-54 US-11-127-877-54 US-11-127-877-54 US-11-127-877-54 US-11-190-188-19 US-11-190-188-19 US-11-190-19-71-18	US-11-087-099-6776 US-11-124-368A-265
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ALIGNMENTS

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RESULT 1
US-11-030-498-36
Sequence 36, Application US/11032498
Sequence 36, Application No. US20050249743A1
Sequence 36, Application No. US20050249743A1
Sequence 36, Application No. US20050249743A1
SEQUENCE INCOMPATION:
SETTLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
TITLE OF INVENTION UNMBER: US/11/032,498
CURRENT FILING DATE: 2005-01-10
PRIOR PELICATION NUMBER: US 60/535,751
PRIOR PELICATION NUMBER: US 60/535,751
SEQUENCE IN NOS: 37
SOFTWARE: PetentIn version 3.2
SEQ ID NO 36
LENGTH: 20
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US-11-155-288-7

is Sequence 7, Application US/11155288

sequence 7, Application No. US20060008468A1

is GENERAL INFORMATION:

is APPLICANT: Chiang, Chih-Sheng

APPLICANT: Simard, John J.L.

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

TITLE OF INVENTION: ANTIGENS US/11/155,288

CURRENT APPLICATION NUMBER: US/11/155,288

CURRENT FILING DATE: 2005-06-17

PRIOR APPLICATION NUMBER: 60/580,969

PRIOR FILING DATE: 2004-06-17

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FASTSEQ for Windows Version 4.0
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RESULT 6
US-11-072-512-2739
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US-11-021-441-28

US-11-021-441-28

US-11-021-441-28

US-11-021-441-28

Sequence 28, Application US/11021441

Publication No. US20050249748A1

GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: COCK, David N.
TITLE OF INVENTION: RECOMBINAT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: RECOMBINAT NUCLEIC ACID MOLECULES,
TITLE OP INVENTION: RECOMBINAT NUCLEIC ACID MOLECULES,
TITLE OP INVENTION: THEREOF
FILE REFERENCE: 28217200390

CURRENT APPLICATION NUMBER: US 60/615,750

PRIOR PILING DATE: 2004-10-01

PRIOR PILING DATE: 2004-00-01

PRIOR PILING DATE: 2004-00-01

PRIOR PILING DATE: 2004-00-01

PRIOR PILING DATE: 2004-00-03

PRIOR PILING DATE: 2004-00-30

PRIOR PILING DATE: 20
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                                                                                                                                                                                        Query Match 100.0%; Score 47; DB 7; Length 180; Best Local Similarity 100.0%; Pred. No. 0.023; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 7; Length 240; 100.0%; Pred. No. 0.032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 412, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                       127 TVSGNILTIR 136
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                    LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-485-517-412
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SEO ID NO 7
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US-11-098-686-10549
US-11-098-686-10549

US-11-098-686-10549, Application US/11098686

PUBLication No. US20060024696A1

GENERAL INFORMATION:

TITLE OF INVENTION: Vivek and Gebhart, Connie J.

TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REPRENCE: 0953-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR PILING DATE: 2003-10-01

PRIOR PILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                          Length 223;
                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                       Query Match 74.5%; Score 35; DB 6; Best Local Similarity 70.0%; Pred. No. 8.1; Matches 7; Conservative 1; Mismatches 5
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 412
LINGHH: 223
                                                                                                                                                                                                                ORGANISM: Staphylococcus epidermidis US-10-485-517-412
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US-11-098-686-10549
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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TAMECHIKA, ICHIRO
SEKI, NAOHIKO
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMO)
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-:
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 6, Conservative
                                              38 TLSGNILII 46
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45 SVAGNIITI
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APPLICANT: WALSH, Roderick T.
APPLICANT: WALSH, Roderick T.
APPLICANT: LO, Terence P.
APPLICANT: LO, Terence P.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REPREBREE: P1-0.044 PCT
CURRENT APPLICATION NUMBER: US/11/190,188
PRIOR APPLICATION NUMBER: US/10/220,382
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
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Pred. No. 40;
1; Mismatches 1; Indels
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                     APPLICANT: OLDOLA, CALLEL APPLICANT: AGGHARI, KENJI
APPLICANT: MAGHARI, KENJI
FELE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2739
LENGTH: 585
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; OTHER INFORMATION: Incyte ID No: 3082743CD1
US-11-190-188-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. TOM
APPLICANT: PATTERSON, Chandra
APPLICANT: YAO, MONIQUE G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: TRIBOULEY, Catherine
APPLICANT: VUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/11190188 Publication No. US20060035331A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHAN, Farrah A.
POLICKY, Jennifer L.
AU-YOUNG, Janice
YANG, Junming
YOSHIKAWA, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                         72.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 TPSGNILTL 395
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US-11-072-512-2739
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LENGTH: 313
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                APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                       APPLICANT: CHIRON Sph
APPLICANT: POTTANA Maria Rita
APPLICANT: FORTANA Maria Rita
APPLICANT: POZZA Mariagrazia
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR RILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 1556
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.2%; Score 33; DB 6; Length 426; 66.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.2%; Score 33; DB 6; Length 387; 77.8%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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US-10-873-528-34

US-10-873-528-34

Sequence 34, Application US/1087528

Publication No. US20050276814A1

GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFRENCE: PWC/P21129W
CURRENT APPLICATION NUMBER: US/10/873,528

CURRENT FILING DATE: 2004-06-23

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: GB 9816337.1

PRIOR FILING DATE: 1999-03-27

PRIOR FILING DATE: 1999-03-19

NUMBER: OF SEQ ID NOS: 388

SEQ ID NO 34
US-10-467-657-1556
Sequence 1556, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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1 TVSGNILTIR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-711
                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-053-076-81
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                                                 Sequence 901, Application US/10995561
Publication No. USZ0050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL,
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASESEQ for Windows Version 4.0
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APPLICANT: Goedegebuur, Frits
APPLICANT: Goedegebuur, Frits
APPLICANT: Gualfetti, Peter
APPLICANT: Gualfetti, Peter
APPLICANT: Mefe, Paulien
APPLICANT: Sandgren, Mats
APPLICANT: Sandgren, Mats
APPLICANT: Sandgren, Mats
APPLICANT: Stahlberg, Jerry
TITLE OF INVENTION: Callulases
FILE REFERENCE: G772-3
FILE REFERENCE: G772-3
FILE REPERENCE: G772-3
FRICH APPLICATION NUMBER: US 60/458,853
FRICH PILING DATE: 2003-08-15
FRICH APPLICATION NUMBER: US 60/458,696
FRICH RILING DATE: 2003-03-27
FRICH APPLICATION NUMBER: US 60/456,368
FRICH APPLICATION NUMBER: US 60/404,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 471;
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Pred. No. 56;
2; Mismatches 2; Indels
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Publication No. US20050277172A1
GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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; ORGANISM: Irpex lacteus
US-10-641-678-47
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CORGANISM: Homo sapiens
US-10-995-561-901
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88 TIAGNILVI 96
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RESULT 10
US-10-995-561-901
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LENGTH: 471
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US-10-485-788A-711, Application US/1048788A
publication (US 20202247431
publication (US 2020227431)
publication (US 202021008)
publication (US 20202108)
publication (US 2020208)
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APPLICANT: Day, Authony, G.
APPLICANT: Goadegeburr, Frits
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchingon, Colin
APPLICANT: Mitchingon, Colin
APPLICANT: Sandgren, Mats
APPLICANT: Sandgren, Mats
APPLICANT: Sandgren, Mats
APPLICANT: Shaw, Andrew
APPLICANT: Staw, Andrew
TITLE OF INVENTION: Ocellulases
TITLE OF INVENTION: Cellulases
TITLE OF ILINGANT: 2003-08-15
CURRENT APPLICATION NUMBER: US 60/458,853
PRIOR APPLICATION NUMBER: US 60/458,696
PRIOR PLING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/456,368
PRIOR FILING DATE: 2003-03-27
PRIOR PLING DATE: 2003-03-27
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/456,368
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
                                                                                                                                                                                    2; Indels
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US-10-467-657-1358
US-10-467-657-1358
is Sequence 1358, Application US/10467657
is Publication No. US20050260581A1
is GENERAL INFORMATION:
is APPLICANT: FONTANA Maria Rita
is APPLICANT: PIZZA Mariagrazia
is APPLICANT: MASIGNANI Vega
is APPLICANT: MANACI Elisabetta
it TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
                                                                                                                                   Score 32; DB 7
Pred. No. 14;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
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Publication No. US20050277172A1
GENERAL INFORMATION:
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ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1358
                                                                                                                                      68.1%;
80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 85.77
Matches 6; Conservative
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; SEQ ID NO 81
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-81
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95 TVSGNVL 101
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Gaps
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PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 523
                                                                                                                                                                                              6; Conservative
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                                                                                    TYPE: PRT ORGANISM: Irpex lacteus
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Matches 6; Conserv
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March 13, 2006, 18:52:59 ; Search time 75.2941 Seconds (without alignments) 58.355 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: geneseqp198
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aay05015 Human can Aay05969 Human can Aab31311 Exemplary Aae07734 Human MHC Abg66802 Tumour an Adg89596 Class I H Aay06066 Human can Aay06066 Human can Aay06066 Human can Aay06066 Human can Aay0606979 Human can Aay05979 Human can Aay05979 Human can Aay05976 Human can Aay05979 Human can Aay05965 Human can Aay05965 Human can Aay02191 Human can Aay030154 Human cun	Amino
SUMMARIES DB ID	2 AAYO6015 2 AAYO6015 4 AAB31331 4 AAB70734 5 AB666802 8 AD6089596 2 AAYO6066 2 AAYO6066 2 AAYO6066 2 AAYO6986 2 AAYO5998 5 AAYO5978 2 AAYO5978 2 AAYO5965 3 AAYO5965 3 AAYO5965 3 AAYO5965 4 AAYO5965 4 AAYO5965 3 AAYO5965 4 AAYO5965 4 AAYO5965 4 AAYO5965 4 AAYO5965 4 AAYO5965 4 AAYO6965	4 AAG67164
Length D	110 110 110 110 111 111 111 1110 1110	180
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Score		55.5
Result No.	1264200001111111111111111111111111111111	24.

Aau01535 Human NY-	Aae07714 Human NY	Aau84818 Human NYN	Aau11543 Human tum	Abr58672 Human can	Abr48210 Human bla	Abu56508 Lung canc	Abu56694 Lung canc	Abp74198 Human NY-	Abu64816 Human NY-	Abr83438 Human NY-	Adc09576 NY-ESO-1	Add35564 Human NY-	Add35568 Human NY-	Add25510 Binding d	_	Adj54139 Human NY-	Adm72815 Human NY-	Adm73418 CAG-3 pro	Adm73417 Human NY-	Adq18451 Human sof
AAU01535	AAE07714	AAU84818	AAU11543	ABR58672	ABR48210	ABU56508	ABU56694	ABP74198	ABU64816	ABR83438	ADC09576	ADD35564	ADD35568	ADD25510	ADN39068	ADJ54139	ADM72815	ADM73418	ADM73417	ADQ18451
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25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX56599) .30 Epitopes (see AAX05988-Y060/17) were identified. The present peptide (ranked 28) corresponds to amino acid residues 53-62 of CAG-1 ORF1 (see AAX05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAX05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-lodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; ervical cancer; cancer; cancer; tuding cancer; cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA. Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif. (USSH) US DEPT HEALTH & HUMAN SERVICES. Example 10; Page 42; 88pp; English. AAY06015 standard; peptide; 10 AA. 98WO-US019609. Cancer antigen NY ESO1/CAG-3. 97US-0061428P (first entry) Wang RF, Rosenberg SA; WPI; 1999-277270/23. Homo sapiens. WO9918206-A2. 21-SEP-1998; 08-OCT-1997; 15-APR-1999. 16-AUG-1999 AAY06015; AAY0601E

AAAY0601E

AAAX0601E

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The present sequence represents a cancer peptide that is based on amino acid residues 55-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-67), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or triunour antigen, antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an Hamble ancer by administering a cancer peptide, with or without and Hamble ancer as such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, lidney cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
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without an HLA molecule. The cancer peptides form part of, or are derived
               from, cancers such as primary or metastatic melanoma, thymona, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NY ESO-1/CAG-3 gene, CAG-3 gene, cancer peptide, antigen, human, leukaemia, non-Hodgkins lymphoma, Hodgkins lymphoma; lung cancer, metastasis, melanoma; adenocarcinoma; thymoma; colon cancer, uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                                                                                                                      Length 10;
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Pred. No. 0.6;
                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                    100.0%;
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                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
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N-PSDB; AAX58600.
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                                                                                                              Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAY05969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine.
                                                                                                                                                                                                                                                                                                                          RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1.
prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                 Exemplary antigen characteristic of tumours and derived from NY-ESO-1.
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                                                                                                                                   Gaps
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                                                                                                  DB 2; Length 10;
                                                                                                                                   Indels
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                                                                                                 100.0%; Score 55; DB 2 100.0%; Pred. No. 0.6;
                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                     AAB31331 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
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Best Local Similarity
                                                                                                                    Best Local Similarity
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                                                                 Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2000.
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                                                                                                 Query Match
                                patient
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human leukocyte antigen, fusion protein, epitope, cytostatic; tumour, gastrointestinal tumour, colorectal cancer, gastro-oesophageal cancer, liver cancer, biliary tract cancer; pancreatic cancer, vaccine;

Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA;

Tumour antigen NY-ESO-1/CAG3 ORF1, HLA-A31 epitope.

(first entry)

24-SEP-2002

ABG66802;

prostatic cancer; testicular cancer; lung cancer; breast cancer; malignant melanoma; mesothelioma; brain tumour; ovarian cancer; uterine cancer; cervical cancer; head and neck cancer; bladder cancer;

Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma; acquired immunodeficiency syndrome; AIDS-related lymphoma

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The invention relates to the identification and isolation of major histocompatibility (WHC) class II restricted T cell epitope (WHC-II epitope) derived from the cancer antigen, NV ESO-I. The MHC-II epitopes (Tom NV ESO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in amammal by aliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is MHC class I restricted human NY ESO-I cancer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.
                                                                                                                                                                                            Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 4; Length 10; 100.0%; Pred. No. 0.6;
                                                                                                                                                       Human MHC class I restricted NY ESO-1 cancer peptide #2.
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                                     AAE07734 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-2001; 2001WO-US002765.
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                                                                                                               06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang R, Rosenberg SA,
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Best Local Similarity
Matches 10, Conserv
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                                                                                                                                                                                                                                                                                immunotherapy
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                                                                           AAE07734;
RESULT 4
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New polynucleotide capable of expressing an epitope-beta2m fusion protein useful for generating cytotoxic T lymphocyte responses against a tumor and in restoring antigen presentation in the tumor of a host.

Hunter M;

Tafuro S, Meier U, Mcmichael AJ, Bell JI, Layton G,

WPI; 2002-508108/54

01-NOV-2001; 2001WO-GB004844. 02-NOV-2000; 2000GB-00026812. (ISIS-) ISIS INNOVATION LTD

WO200236146-A2.

10-MAY-2002.

Homo sapiens.

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The invention relates to a new polynucleotide capable of expressing an epitope-beta 2m fusion protein useful for generating cytotoxic T lymphocyte (CTL) responses against a tumour or in restoring antigon presentation in the tumour of a host. Also included are a polynucleotide capable of expressing an epitope-beta_2m fusion protein in combination with a vaccination agent that stimulates a CTL response against the epitope of the fusion protein for simultaneous, separate or sequential use in the treatment of cancer and a method of treating a tumour by administering a capable of expressing an epitope-beta_2m fusion protein, and optionally a vaccination agent that stimulates a CTL response against the epitope of the fusion protein. The polynucleotide is useful for generating CTL responses against tumours, for restoring antigen as gastration in the tumour, and subsequently for treating cancer, such as gastration in the tumour, prostatic, testicular, lung or breast cancer, malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine as gastrointestinal tumour, prostatic, testicular, lung or breast cancer, cancer including cervical cancer, cancer of the head and neck, bladder cancer, Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and heamstopoletic malignant tumours such as leukaemia and lymphoma. The heatened sactioned is a thmour antigen. The present sequence is a tumour HLA epitope used in the fusion proteins of the invention
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Best Local Similarity 100.
Matches 10; Conservative
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RESULT 6

ABG66802 standard; peptide; 10 AA.

RESULT 5 ABG66802

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Gaps

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Mismatches

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Conservative

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1 ASGPGGGAPR 1 ASGPGGGAPR

ADG89596

us-09-529-206e-25.rag

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New vaccine composition comprises inverted microsomes from animal cells with an externally disposed peptide antigen and a protein of the Major Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                       (or its membrane fragments), in peptide antigen and a protein of
                                                                                                                                                                                                                                                                                                                                                                                                              inverted microsomes from an animal cell (or its membrane fragments), in the mesociation with an externally disposed peptide antigen and a protein of the MHC. The vaccine composition of the invention is useful for the prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast, fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The present amino acid sequence represents a class I HLA-restricted cancer antigen which was found to be expressed by normal spermatocytes and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-lodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; ervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                 invention comprises a vaccine composition that consists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 9; Length 10; 100.0%; Pred. No. 0.6;
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                                                                                                                       (UNLO ) QUEEN MARY & WESTFIELD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 48; 83pp; English
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                                         30-JUL-2004; 2004WO-GB003285
                                                                              01-AUG-2003; 2003GB-00018096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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10-FEB-2005
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                                                                                                                                                                 Wang P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a cell that differentiates into a metastatic cancer cell, useful for preventing metastatic cancer, comprises identifying a mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises a method for identifying a cell that will differentiate into a metastatic cancer cell, the method involves identifying a mutated fibronectin in the cell. The method of the invention is useful for preventing metastatic cancer. The present amino acid sequence represents a Class I HLA-restricted testis cancer antigen.
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                                                                                                                                                                                metastatic cancer cell differentiation, mutated fibronectin, metastatic cancer; class I HLA-restricted; testis; cancer antigen.
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                                                                                                                                             Class I HLA-restricted testis cancer antigen #31
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                   ADG89596 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                           28-MAY-2003; 2003WO-US016736.
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Les 10; Conserv
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                                                                                                                       This peptide corresponds to amino acid residues 53-63 of human NY ESO-1/CAG-3 ORF1 (see AAV05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAV0567-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This peptide corresponds to amino acid residues 52-62 of human NY BSO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                               as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                                        Example 11; Page 50; 88pp; English.
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                                                     Cancer antigen NY ESO1/CAG-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASGPGGGAPR
                 WPI; 1999-277270/23.
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Best Local Similarity
Matches 10; Conserv
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preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide corresponds to amino acid residues 51-62 of human NY ESO-1/CAG-3 ORF1 (see AAYO5965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAYO5967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HiA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                                                                                                                            100.0%; Score 55; DB 2; Length 11; 100.0%; Pred. No. 0.66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer antigen NY ESO-1/CAG-3 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                       AAY06065 standard; peptide; 12 AA.
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                                                                                                                                                                                              Local Similarity
                                                                                                                                         Sequence 11 AA;
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The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAVOS955), a new and potent tumour antiquen capable of eliciting an antiquen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAVOS956), portions of them and their variants (see AAVOS95-187), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods concer peptide, useful in diagnostic and detection assays; and methods of the remover peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, Imng cancer, liver cancer, leukaemia, uterine cancer, lymphoma, sercoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine cancer, lymphoma breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                           NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; prostate cancer; ovarian cancer; ervical cancer; bladder cancer; kidney cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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16-AUG-1999 (first entry)
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                  Homo sapiens
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AAY05978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide corresponds to amino acid residues 50-62 of human NY ESO-
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                                                                                                                                                                                                                                                                                                                                         Human cancer antigen NY ESO-1/CAG-3 peptide.
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                                                                                                                                                                                          AAY06064 standard; peptide; 13 AA
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Matches 10; Conserv
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The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAVO5965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF2 (see AAVO5966), portions of them and their variants (see AAVO59-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods correr peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods or preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, inver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
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                                                              uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
NY ESO-1/CAG-3 gene, CAG-3 gene, cancer peptide, antigen, human,
leukaemia, non-Hodgkins lymphoma, Hodgkins lymphoma, lung cancer,
metastasis, melanoma, adenocarcinoma, thymoma, colon cancer,
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Matches 10; Conservative
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                                                                                                                                                                          Homo sapiens.
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The present sequence represents a cancer peptide that is based on amino acid residues 44.62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY0565), a mew and potent tumour antigen capable of elicting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 3 ORF2 (see AAY05966), portions of the cancer. The cancer and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antibodies reacting with a CAG-3 cancer peptide, or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, concers such as ministering a cancer peptide, with or without an cancer such as primary or metastatic melanoma, thymoma, lymphoma, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancers bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer, specific T cells in vitro for subsequent return to a
cervical cancer, bladder cancer, kidney cancer, pancreatic cancer,
liver cancer, sarcoma, tumour, diagnosis, immunotherapy, therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; diardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU85105 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                98WO-US019609.
                                                                                                                                                                                                                                                    97US-0061428P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NYNSOla segment 4.
                                                                                                                                                                                                                                                                                                                              Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
                                                                              Homo sapiens.
                                                                                                                                    WO9918206-A2
                                                                                                                                                                                                              21-SEP-1998;
                                                                                                                                                                                                                                                    08-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                                                                          15-APR-1999.
                                                                                                  Synthetic.
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                                    vaccine
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Gaps

us-09-529-206e-25.rag

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PW W0200190197-A1.

PD 29-NOV-2001.

EX 29-NOV-2001.

EX 25-NOV-2001.

EX 26-NOV-2000.

EX
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Oy 1 ASGPGGGAPR 10 |||||||||| ||| ASGPGGGAPR 19

; 0

0; Gaps

Query Match 100.0%; Score 55; DB 5; Length 30; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 10; Conservative 0; Mismatches 0; Indels

Search completed: March 13, 2006, 19:03:58 Job time : 77.2941 Becs

Tue Mar 14 10:35:53 2006

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

March 13, 2006, 19:04:24; Search time 11.8824 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-25 55 1 ASGPGGGAPR 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pirl:* 3: pir2:* 4: pir3:* PIR 80:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dip				
Result		Query				
No.	Score	Match	Match Length	DB	ID	Description
		1		١,		
-	44	80.0	3190	N	T13828	CREB-binding prote
7	42	76.4	378	N	C87425	aldose 1-epimerase
m	41	74.5	173	~	AB3648	flagellar basal-bo
4	41	74.5	286	~	S04673	H+-transporting tw
D.	41	74.5	357	7	F82878	XAA-PRO aminopepti
9	41	74.5	1207	7	T00378	KIAA0641 protein -
7	40	72.7	335	7	S08341	myristylated alani
ω	40	72.7	436	~	T36104	conserved hypothet
6	40	72.7	521	~	A29345	steroid hormone re
10	40	72.7	619	~	802165	regulatory protein
11	40	72.7	954	~	A87431	
12	39	70.9	103	~	C72683	ര
13	39	70.9	114	~	B45036	Pur beta - human (
14	39	70.9	163	~	E87464	competence/damage-
15	39	70.9	166	7	169006	histocompatibility
16	39	70.9	187	~	T35619	hypothetical prote
17	39	70.9	260	7	F95899	_ ⊆
18	39	70.9	466	7	F95307	conserved hypothet
19	39	70.9	474	~	G75580	conserved hypothet
20	39	70.9	999	~	T34842	probable transfera
21	39	70.9	575	~	835327	protein kinase sgg
22	39	ö	627	~	T35608	polyketide hydroxy
23	39	70.9	733	N	S10932	probable protein k
24	39	ö	757	~	JC7726	(1->4)-alpha-D-glu
25	39	70.9	1028	7	A56038	DNA-binding protei
56	39		1067	~	S35423	protein kinase sgg
27	39	•	1213	7	S16356	ovo protein - frui
28	39	70.9	1317	~	T03748	
29	38	69.1	131	~	C75445	Pex-related protei

anther-specific pr	Hypothetical Prote	hypothetical prote	alternative splici	alternative splici	alternative splici	related to antifre	alternative splici	proline iminopepti	hypothetical prote	POU-domain protein	hypothetical prote	syntaxin synt4 (im	class I histocompa	hypothetical prote	octamer binding tr
812246	AE3136	G98151	C40040	S26404	A40040	T51008	B40040	AC1965	T29031	S78452	T08459	T48847	180170	T30168	159234
~	7	~	~	~	7	~	~	7	7	~	~	~	~	~	0
161	189	189	201	201	248	286	292	316	327	331	341	341	354	397	420
69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1
38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

T13828 CREB-binding protein homolog - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R;Akimaru, H; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G
Nature: 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Accession: T1328
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 A&XI>
A;Residues: 1-3190 A&XI>
C;Genetics:

Cyconstruction: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>

Gaps °, Length 3190; Query Match 80.0%; Score 44; DB 2; Length 319 Best Local Similarity 77.8%; Pred. No. 1.8e+02; Matches 7; Conservative 1; Mismatches 1; Indels

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:||||| || 320 NGPGGGGPR 328 2 SGPGGGAPR 10

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C;Genetics: A;Gene: CC1418 C;Superfamily: aldose 1-epimerase

76.4%; Score 42; DB 2; Length 378; 77.8%; Pred. No. 56; Query Match Best Local Similarity

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A;Residues: i-1207 <ISH>
A;Cross-references: UNIPARC:UPI000046CF7; EMBL:AB014541; NID:93327095; PIDN:BAA31616.1.,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myristylated alanine-rich protein kinase C substrate - bovine
NyAlternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
(Species Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: 808341; A32904; $29270; A46098; PS0338
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1887
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinas
A;Reference number: 808341; MUID:89282412; PMID:2734111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-335 <STU>
A;Cross-references: UNIPROT:P12624; UNIPARC:UP1000016C340; EMBL:M24638; NID:g163339; PII
A;Cross-references: UNIPROT:P12624; UNIPARC:UP1000016C340; EMBL:M24638; NID:g163339; PII
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
A;Title: Molecular cloning, Characterization, and expression of a cDNA encoding the "80-A;Reference number: A32904; MUID:89264553; PMID:2726763
              A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI0000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN
C;Genetics:
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C,Date: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Residues: 1-98,'Q',100-335 <ST2>
A;Cross-references: UNIPARC:UP1000017750A; GB:M24638; GB:M23738
                                                                                                                                                                                                                                                                                                                                Length 357;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                   .,
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                                                                                                                                                                                                                   A,Gene: pepp, UUS32
A,Genetic code: SGC3
C,Superfamily: X-Pro aminopeptidase
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nes 7; Conserv
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                                                                                                                                                                                                                                        flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
(Species: Brucella melitensis
(Species: Abasella melitensis)
(Species: Abasella melitensis)
(Species: Mazur, M.; Goltsman, B.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
(A.Reference number: Abasella melitensis)
(A.Reference number: Abasella melitensis)
(A.Reference number: Abasella melitensis)
(A.Residues: Dreliminary
(A.Residues: 1-173 < KUR>
(A.Residues: 1-173 < KUR>
(A.Residues: 1-173 < KUR>
(A.Residues: 1-173 < KUR>
(A.Residues: Brain 16M)
(C.Genetics: Strain 16M)
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C; Accession: F82878
R; Glass, O.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rhodopseudomonas Diastica
C;Accession: 07-89-1990 #text_change 31-Dec-2004
C;Accession: 504673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179; 185-214, 1984
A;Title: Rhodopseudomonas Diastica atp operon. Nucleotide sequence and transcription. A;Reference number: 50466; MUID:85058188; PMID:6209404
A;Reference number: 80466; MUID:85058188; PMID:6209404
A;Accession: 804673
A;Actual: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 4TMS
A;Residues: 1-286 4TMS
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex
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Pred. No. 61;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.5%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 40; Matches 7; Conservative 0; Mismatches
Mismatches
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80.0%;
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7; Conservative
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                                                                                   :|| |||||
282 NGPSGGAPR 290
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                                                      2 SGPGGGAPR 10
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Best Local Similarity
Matches 8; Conserv
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A; Map position: II
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Matches
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N.Alternate names: estrogen-related receptor
C;Species: Homo sapiens (man)
C;Accession: A29345; A49074
R;Giquere, V.; Yang, N.; Sequi, P.; Evans, R.M.
Nature 31, 91-94, 1988
A;Atitle: Identification of a new class of steroid hormone receptors.
A;Reference number: A29345; MUID:88122546; PMID:3267207
A;Accession: A2945
A;Accession: A294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory protein flay - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: 802165
R;Kaplan, J:B:/ Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
J. Mol. Biol. 205, 71-83, 1989
A;Ritler Temporal regulation and overlap organization of two Caulobacter flagellar gene
A;Reference number: S02164; MUID:89178645; PMID:2648000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulatory protein FlaEY [imported] - Caulobacter creecentus
C;Species: Caulobacter creecentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Rosidues: 166-169, X/,171-173 <WIL>
A;Rosidues: 166-169, X/,171-173 <WIL>
A;Coss-references: UNIPARC:UPI000017AlDF
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; F;174-434/Domain: erbA transforming protein homology <ERBA>
F;176-196/Region: zinc finger
F;212-236/Region: zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 2; I
Pred. No. 1.4e+02;
1; Mismatches 1;
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77.88;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                        steroid hormone receptor ERR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 AGGPGAGAP 181
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Best Local Similarity
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                                                                                                                                                                                                                               A.Molecule type: DNA
A.Residues: 191-253, SEE', 257-279, 283-292, 'V', 294, 'PEQE', 299, 'A', 300, 'A', 302-313, 'A', 315
A.Cross-references: UNIPARC:UPI000017750B
R.Manentl, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
B. Biol. Chem. 268, 6878-6881, 1993
A.Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A.Reference number: A46098; MUD:93216617; PMID:8463217
R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protei
or equivalent genes in different species.
A;Reference number: S29267; MUID:93011168; PMID:1396720
A;Accession: S29270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000017750C
R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Bocchem. Biophys. Res. Commun. 182, 1355-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
A;Reference number: PS0338; MUID:92171958; PMID:1540183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750B; UNIPARC:UPI000017750F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: brain
A, Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs C; Comment: This protein is a major cellular substrate for protein kinase C and plays a r C; Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: neurofilament triplet H protein
C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT: O8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A;Reference number: 221597
A;Reference number: T36104
A;Accession: T36104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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Pred. No. 98;
1; Mismatches (
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Best Local Similarity 64.3%;
Matches 9; Conservative 1
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 2-11 < MAN>
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Best Local Similarity
Matches 7; Conserv
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R.Boyson, J.E.; McAdam, S.N.; Gallimore, A.; Golos, T.G.; Liu, X.; Gotch, F.M.; Hughes, Immunogenetics 41, 59-68, 1995

Aftitle: The MHC E locus in macaques is polymorphic and is conserved between macaques at A; Reference number: I54551; MUID:95104933; PMID:7806297

A; Accession: I69006
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-166 <RES.
A;Cross-references: UNIPROT:Q95518; UNIPARC:UPI00000892D6; EMBL:U02981; NID:g512971; PII
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 169006
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CjSpecies: Homo sapiens (man)

CjDate: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

CjAccesion: B45036

R;Bergemann, A.D.; Ma, Z.W.; Johnson, B.M.

Mol. Cell. Biol. 12, 5573-5682, 1992

A;Title: Sequence of cDNA comprising the human pur gene and sequence-specific single-stransparence number: A;5036; MUID:93078769; PMID:1448097

A;Reference number: A;5036; MUID:93078769; PMID:1448097

A;Recession: B45036

A;Return: preliminary; not compared with conceptual translation

A;Residues: 1-114 vBER-
A;Cross-references: UNIPROT:096QR8; UNIPARC:UPI000017C32D

A;Experimental source: HeLa cells
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon I. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Froc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2011
A.; Title: Complete Genome Sequence of Caulobacter crescentus.
A.; Reference number: A87249; MUD: 21173698; PMID: 11259647
A.; Residuan ary
A.; Residuatus: preliminary
A.; Residuatus: preliminary
A.; Residuatus: 1-954 <STO>
A.; Cross-references: UNIPROT: P15345; UNIPARC: UPI000012ABED; GB: AE005673; NID: 913422833; F.C. Genetics:
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3.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, Y.; Jin-no, K.; Takahayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahayasi, Y.; Jin-no, K.; Takahayasi, Y.; Jin-no, K.; Takahaya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz A.Reference number: A72450; MUID:99310339; PMID:10382966

A.Accession: C72683

A.Status: preliminary
A.Residusa: DNA
A.Residusa: 1-103 < KAW>
A.Cross-references: UNIPROT:Q9YDNO; UNIPARC:UPIO0005DD18; DDBJ:AP000060; NID:g5104188; C;Genetics:
A.Accession: A.Accession: A.Accession Accession Access
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Accession: C72683
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Pred. No. 2.4e+02;
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Pred. No. 49;
1; Mismatches 0; Indels
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85.7%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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70.9%; Score 39; DB 2; Length 166; 77.8%; Pred. No. 74; 2; Indels :ive 0; Mismatches 2; Indels

2

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Competence/damage-inducible protein CinA [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: B87464
C;Accession: B87464
B;Knierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A.Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9A716; UNIPARC:UPI00000C74AD; GB:AE005673; NID:g13423155; P
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Best Local Similarity 75.0%;
Matches 6; Conservative 1
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A,Molecule type: DNA
A,Residues: 1-163 <STO>
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97.196 Million cell updates/sec
                                                                            March 13, 2006, 18:53:23 , Search time 72.5882 Seconds
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Q69pj1
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Q6ypc1
Q6uu54
Q67pj0
Q98p09
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Q8IVQ3 HUMAN
Q7NWI2 CHRVO
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Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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neurospora
aspergillus
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
M. A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";
      oryza
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15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen IB (Autoimmunogenic cancer/testis antigen NY-
                                                                                                 homod
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                                                                              Q5bev2
Q6zv16
Q5x416
Q5vuq8
Q4fkf7
Q4sw43
Q96bu2
Q4syu9
Q4tgy6
Q6uu52
Q4ilq5
Q96tz3
Q4wrl3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 100.0%; Score 55; DB 2; Length 142; Local Similarity 100.0%; Pred. No. 1.6; les 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lethe B.G.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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06UU52_ORYSA
Q41LQ5_G1BZE
Q4RZ3_BBUCR
Q4WR13_ASPFU
Q5ZV16_HUMAN
Q5ZV16_HUMAN
Q5K4L6_HUMAN
Q5K4L6_HUMAN
Q5K4L6_HUMAN
Q4FKF7_9TRYP
Q4FKF7_9TRYP
Q4SVQ2_HUMAN
Q4SWQ3_HUMAN
Q4SWQ3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CTAG1B; Synonyms=CTAG, CTAG1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                        OSNY13 HUMAN PRELIMINARY;
OSNY13 HUMAN PRELIMINARY;
O1-0CT-2000 (TrEMBLRE1 15, LA
O1-0CT-2002 (TrEMBLRE1 22, LA
Hypothetical protein LAGE-2 (F
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62
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                                                                                                     NUCLEOTIDE SEQUENCE
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                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Nelson D.L.;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen 1-A).
Name=CTAG1-B; Synonyme=CTAG1-A, LAGE-2;
Homo sapiens (Huwan)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Evarchontoglires; Primates; Catarrhini; Hominidae;
                                                  Lethe B., Iucas S., Michaux I., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T., "LAGE-1, a new gene with tumor specificity."; Int. J. Cancer 76:903-908(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                         MEDLINE=9843062. PubMed=9759882;
Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
Schwartzentruber D.J., Rosenberg S.A.;
A breast and melanoma-shared tumor antigen: T cell responses to
antigenic peptides translated from different open reading frames.";
J. Immunol. 161:3556-3606(1998).
--- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
variety of cancers. Detected in uterine myometrium.
--- SIMIARITY: Belongs to the CTAG family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.A.Y.-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 1; Length 180; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galgoczy P., Rosenthal A., Platzer M.; "Human-mouse comparative sequence analysis of the NEMO gralternative promoter within the neighboring G6PD gene."; Gene 271:93-98(2001).
                                                                                                                                                                                                                                                                                                                                                                                              Gly-rich.
Bl22C5C2C8BE1569 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997)
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                                                                                                                                                                                                                                                                                                                                                                                    Potential.
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EMBL; AF038567; AAD05202.1; -; mRNA.
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                                            MEDLINE=98289662; PubMed=9626360;
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                                                                                                                                                                                                                                                                                                                                                                                                          180 AA; 17992 MW;
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100.0%;
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Q7LBY4;
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Best Local Similarity 100.
Matches 10; Conservative
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                      CLEOTIDE SEQUENCE.
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                                   TISSUE=Melanoma;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=98289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen E., Boon T.,
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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"Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99325550; PubMed=10399963; Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.; Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.; "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, unexpected translation product of LAGE-1."; Int. J. Cancer 82:442-448(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 2; Length 180; 100.0%; Pred. No. 2; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAG2 HUMAN STANDARD; PRT; 210 AA. 075638; 075637; Q9BU80; Q9UJ88; Q9Y479; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) 10-MAY-2005 (Rel. 47, Last annotation update) Mame=CTAG2; Synonyms=ESO2, LAGE1; Protein) (ESO-2 protein) Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lethe B.G.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF277315; AAL27014.1; -; Genomic_DNA. EMBL; AJ278977; CAB76943.1; -; Genomic_DNA. EMBL; AZ77315; AAL27013.1; -; Genomic_DNA. EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
                                                                                                                                                                                                  Platzer M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                FIGURER M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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MEDLINE=99454989; PubMed=10523621;
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                                               A MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altaener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altaener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altaechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Heish F.,
Brownstein M.J., Usdin T.B., Toshiyuki S.I., Carninci P., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcyan B.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketterman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Manner A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQRPĞTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=LAGB-1A; Synonyms=LAGB-1S;

Isold=075638-2; Sequence=VSP 004301;

TISSUE SPECIFICITY: Testis and very low level in placenta and in

some uterus samples. Observed in 25-50% of tumor samples of

melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: A transmembrane domain is present in isoform LAGE-1A. SIMILARITY: Belongs to the CTAG family.
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Pred. No. 36;
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/FTId=VAR 007857.
8BE0EE00AE55E8BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
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/FTId=VAR_007856.
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R -> 0
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EMBL, AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL, AJ223040; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
EMBL, AJ012834; CAA10194.1; -; mRNA.
EMBL, AJ012835; CAA10194.1; -; mRNA.
EMBL, BC002835; AH028313.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=LAGE-1B; Synonyms=LAGE-1L;
IsoId=075638-1; Sequence=Displayed;
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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Best Local Similarity
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Termination M. T. C. Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., A Atkins T. Crosman L.C., Pit T., Churcher C., Mungall K.L., Bentley S.D., Sebainha M., Thomson N.R., Bason N., Beacham I.R., Bencks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Croninh A., Crossett B., Davis P., DeShazer D., A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., A Rabbinowitech B., Rutherford K., Sanders M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J., M., Chonnia, Disticity of the causative agent of melioidosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pubbled=15377793; DO1=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
                                                                                                                                                                                                                               OrderedlocusNames=BPSS2331;
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%; Score 46; DB 2; Length 327; 88.9%; Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Lipoprotein.
SEQUENCE 327 AA; 33687 MW; AC5D2C7CC4A44A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia pseudómallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL. BX571966; CAH39817.1; -; Genomic_DNA.
GO; GO:0016620; C:membrane; IEA.
                                                                                                                                         Last sequence update)
Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                     327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 AA
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                                         PRT;
                                                                                                          Created)
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                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                   25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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OrderedLocusNames=BMAA2092;
                                     BURPS PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q629N3 BURMA PRELIMINARY;
Q629N3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 AGGPGGGAP 251
                                                                                                                                                                                                       Putative lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                     <u>об</u>знт9_в
обзнт9;
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0629N3 BUT
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Gaps

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1; Indels

Pred. No. 36; 0; Mismatches

9; Conservative

Matches

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Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
Thouse T. Structural flekibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).

BMBL; CP000011; ABU47030.1; -; Genomic_DNA.

CO; GO: O016020; C:membrane; IEA.

R InterPro; IPR007428; VacJ.

R InterPro; IPR007428; VacJ.

R Pfam; PP0433; VacJ; 1.

R Pfam; PR0433; VacJ; 1.

R Pfam; PR04185; VACJINOPPOT.

R Complete proteome; Lipoprotein.
Complete proteome; Lipoprotein.
SEQUENCE 330 AA; 33977 MW; 2F12165CD7366835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSTRAIN-JEGGING TO THE STRAIN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptococcus neeformans var. neoformans JEC21.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=214684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.6%; Score 46; DB 2; Length 330;
88.9%; Pred. No. 78;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Actin Cross-linking, putative.
ORFNames=CNC06000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               708 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001589; Actnin actin bd.
InterPro; IPR001715; Calponin act_bd.
InterPro; IPR011992; EF-Hand type.
InterPro; IPR002017; Spectrin.
Pfam, PF00307; CH; 2.
SWART; SW00033; CH; 2.
PROSITE; PS00019; ACTININ 1; UNKNOWN 1.
PROSITE; PS00020; ACTININ 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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QSKJMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 AGGPGGGAP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ASGPGGGAP 9
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                            Gaps
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25-0CT-2004 (TYEMBLrel. 28, Last sequence update)
25-0CT-2004 (TYEMBLrel. 28, Last sequence update)
25-0CT-2004 (TYEMBLrel. 28, Last annotation update)
Putrescine transport system permease protein.
Name=potI; OrderedLocusNames=BPSS0464;
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Burkholderiaceae; Burkholderia pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 708;
                                                      Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.6%; Score 46; DB 2; Length 708
88.9%; Pred. No. 1.7e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 protein.
708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;
Complete proteome.
SEQUENCE 708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;
                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
                                                    83.6%; Score 46; DB 2; 1
88.9%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                    708 AA.
                                                                                          0; Mismatches
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PROSITE; PS00020; ACTININ 2; UNKNOWN 1.
PROSITE; PS50021; CH; 2.
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                                                                                                                                                                                                                                                11 CRYNE
QŠSWM1 CRYNE PRELIMINARY;
QSSWM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QG3N33 BURPS PRELIMINARY;
QG3N33;
                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                    47 AGGPGGGAP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 AGGPGGAP 55
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                                                                                                                                  1 ASGPGGGAP 9
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                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=283643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=CNBC1180;
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SEQUENCE 70
                                                        Query Match
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GO:0006260; P:DNA replication; IEA.
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                                                                                                                                                                                                                          Q62H22_BURMA_PRELIMINARY;
Q62H22;
                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                        |:|||| |||
350 AAGPGGDAPR 359
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                                                                                                                                            1 ASGPGGGAPR 10
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                                                         Complete proteome. SEQUENCE 362 AA;
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                                                                                             Query Match
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ID 0400P8_HU

AC 0400P8_F

DT 13-SEP-2C

DT 13-SEP-2C

DT 13-SEP-2C

DT 13-SEP-2C

DT 13-SEP-2C

DT NAME=PTGS
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A Atkins T., Croapana L.C., Pitt T., Churcher C., Mungal R.L.,
A Atkins T., Croapana L.C., Pitt T., Churcher C., Mungal R.L.,
Bencley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Bencley S.D., Sebaihia M., Crossett B., Davis P., DeShazer D.,
Chillingworth T., Cromin A., Crossett B., Davis P., DeShazer D.,
A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Rebinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songsivial S., Stewans K., Tunapa S., Vesaratchavest M.,
Whitehead S., Yasts C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melioidosis,
Burkholderia pseudomallei.",
Proc. Natl. Acad. Sci. U.S.A. 101:14240-1425 (2004).
R EMBL; BX571965; CAH35046.1, -; Genomic DNA.
GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
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Burkholderiaceae, Burkholderia, pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                              Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                        309 AA; 33544 MW; 379E21B5B31CDE30 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QG3QTB_BURPS PRELIMINARY; PRT; 362 AA.
63QTB;
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative DNA polymerase III.
OrderedLocusNames=BPSIL2936;
                                                                                                                                                                                                                                 Bystem permease family.

EMBL; BX511966; CAH37920.1; -; Genomic_DNA.
GO; GO:0016021; c:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
InterPro; IPR000515; BPD_transp.
PROSITE; PS50928; ABC_IM1; 1.
                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 45; DB 2;
88.9%; Pred. No. 1e+02;
            PubMed=15377794; DOI=10.1073/pnas.0403302101;
                                                                                                                                                                                                                                                                                                                                             Complete proteome; Transmembrane; Transport
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 SGPAGGAPR 295
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                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-0CT-2004 (TEMBLIE). 28, Last sequence update)
25-0CT-2004 (TEMBLIE). 28, Last annotation update)
DNA polymerase III, delta subunit (EC 2.7.7.7).
Name=holA; OrderedLocusNames=BMAA451;
Burkholderia mallei (Pseudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderianes, NCBI_TaxID=13373;
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InterPro; IPR005790; DNA pol1II delta.
Pfam; PF06144; DNA pol3 delta; I.
TIGREAMS; TIGR01128; DolA, 1.
TIGREAMS; TIGR01128; DolA, 1.
Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                           81.8%; Score 45; DB 2; Length 362; 80.0%; Pred. No. 1.2e+02;
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80.0%; Pred. No. 1.2e+02;
ive 1; Mismatches 1; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                          1; Mismatches
InterPro; IPR010372; DNA_pol3_delta.
InterPro; IRR005790; DNA_pol1II_delta.
Pfam; PP06144; DNA_pol3_delta; I
TIGRFAMS; TIGR01128; holA; 1.
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                                                                                                                                                               362 AA; 38726 MW;
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Q4QQP8;
13-SEP-2005 (TrEMBLrel. 31, Li
13-SEP-2005 (TrEMBLrel. 31, Li
13-SEP-2005 (TrEMBLrel. 31, Li
PTGFRN protein (Fragment).
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                   SEQUENCE
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Matches
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bate N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bate N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bate N.K.,
Antichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwam P.J., McKernan R.J., Malk J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S. N., Krzywinski M.I., Skalaka W.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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US DOE Joint Genome Institute (JGI-PGF);
COPPIND A. Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck G., Richardson P.;
"Remnendor of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                               TISSUE=PCR rescued clones;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales, Cystobacterineae, Myxococcaceae, Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 45; DB 2; Length 788
88.9%; Pred. No. 2.6e+02;
.ive 0; Mismatches 1; Indels
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         788 AA; 88279 MW; F49E034EE2D3603B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Translation initiation factor 2
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 5.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
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Homo sapiens (Human)
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Matches 8; Conserv
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                                                    NCBI_TaxID=9606 i
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Gaps
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                                                                                           Larimer F., Land M.; "Annotation of Anaeromyxobacter" Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arthrobacter 1824.
Batteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micrococcineae, Micrococcaceae, Arthrobacter.
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                                                                                                                                                                                                                                                                                                                                                                                     Length 262;
                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 2; Length 262
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
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                                                                                                                                               dehalogenans 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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EMBL; AAHGO1000033; EAL94269.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 271 AA; 29989 WW; SECC048B06CDDSBA CRC64;
                                                                                                                                                                                                                                                                                                                                    262 AA; 25294 MW; 7EF93CC8DE0B47FF CRC64;
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Last annotation update)
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87.5%; Pred. No. 1.3e+02;
cive 1; Mismatches 0;
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STRAIN=FB24;
US DOE Joint Genome Institute (PGF-ORNL);
                                                                         US DOE Joint Genome Institute (JGI-ORNL);
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US DOE Joint Genome Institute (JGI-PGF);
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QGAV33 ORYSA
ID QGAV33_ORYSA PRELIMINARY;
AC QGAV33;
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nes 7; Conservative
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ORFNames=ArthDRAFT_03
                                                                                                                                                                                                                                                           preliminary data.
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[2]
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                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                            Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Haiso J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., White O., Salzberg S.L., Fraser C.M., Fraser C.M., Salzberg S.L., Fraser C.M., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 44; DB 2; Length 367;
80.0%; Pred. No. 1.7e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Buell R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
Gramen; O6A733; -.
Hypothetical protein.
SEQUENCE 367 AA; 37474 MW; BBCG2D9D4CC18C86 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0063J18.9.
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Matches 8; Conservative
                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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 STATE:
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Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 32326, A
Sequence 117, App
Sequence 117, App
Sequence 117, App
Sequence 117, App
Sequence 1759, A
Sequence 1759, A
Sequence 1759, A
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 8, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 9, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 3, Appli
Sequence 562, App
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Sequence 6, Appli
Sequence 43766, A
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                                                                             March 13, 2006, 19:14:49; Search time 18.5882 Seconds (without alignments) 44.477 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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US-09-751-798-8

US-09-341-828-9

US-09-341-829A-9

US-09-341-829A-7

US-08-791-495-5

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-355-991A-17349

US-09-252-991A-17249

US-09-252-991A-17249
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US-09-270-767-43766
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                    572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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                                                                                                                             US-09-529-206E-25
55
                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                             Perfect score:
                                                                                                                                                          Sequence:
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                                                    Sequence 31361, A Sequence 16, Appl Sequence 1964, App Sequence 11, Appl Sequence 20489, A Sequence 15052, A Sequence 6, Appli Sequence 7812, A Sequence 7812, A Sequence 2, Appli Sequence 18, Appli Sequence 18, Appli
                                                                       16, Appl
376, App
19543, A
   3369, Ap
27111, A
32992, A
31361, A
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                      Sequence
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US-10-104-047-3369
US-09-252-991A-27111
US-09-252-991A-31391
US-09-252-991A-31361
US-09-08-600B-16
US-05-949-002-376
US-09-248-796A-19643
US-09-248-796A-19643
US-09-252-991A-20489
US-09-902-540-12423
US-09-902-540-12423
US-09-902-540-1262
US-09-902-540-1262
US-09-902-540-1262
US-09-903-106-7062
US-09-904-016-7062
US-09-904-016-7062
US-10-088-045-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTY PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESSEDNDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                           US-08-836-620A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212.
REFERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELEFANS: 617-720-3500
TELEFANS: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 9, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
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amino acid
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Matches 10; Conservative
   MOLECULE TYPE: protein
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CLASSIFICATION: 435
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Matches
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      Sequence 8, Application US/08937263B
Sequence 8, Application Sequence 1
GENERAL INFORMATION:
APPLICANT: Gene, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gene, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Glevander, Knuth; Dijfhout, Jan W.
TITLE OF INVENTION: INSOLATED NOLECULE
TITLE OF INVENTION: ITSELF, AND USES THEREOF
TITLE OF INVENTION: ITSELF, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STATE: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
APPLICANT: Knuth, Alexander; Old, Lloyd J.
APPLICANT: Knuth, Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET 666 Fifth Avenue
CITY: New York CLty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10103
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent REGISTRATION NUMBER: 40,177
REGISTRATION NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %5-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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US-08-937-263B-8
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Gaps
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; Sequence 25, Application US/09392714A
; Patent No. 6680147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; TITLE OF INVENTION: Therefor
; TITLE REFERENCE: LO46,1/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT PILING DATE: 1998-09-09
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NOS: 30
; SEQ ID NO SE: 30
; IRNOTEL 106
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION NUMBER: 08/725,182
APPLICATION NUMBER: 08/725,182
APPLICATION NUMBER: 08/725,182
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
RECISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 318-3168
                                                                                                         COPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-392-714-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYPE: amino acid
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Best Local Similarity
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      <151> 1998-01-27
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Pred. No. 2.7;
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APPLICANT: Ducas, Sophies
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/09849602

Patent No. 6794501

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Teng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105(JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER: PATENTIN VOS: 30

SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                      NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
    PRIOR APPLICATION NUMBER: PCT/US98/01445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; SCUL
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 Atlantic Avenue
                                                                                                                                                                                                                          10; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                  1 ASGPGGGAPR 10
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                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                   Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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STREET: bv.
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LENGTH: 180
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                                                                                   LENGTH:
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                                                                                             APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 2; Length 180; 100.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Thierry
TITLE OF INVENTION: LAGS-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE REFERENCE: LO461/706 (S/09/341,829A
CURRENT APPLICATION NUMBER: US 08/791,495 <151> 1997-0
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION: DATA:
                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING: DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hanson, No. 6723832man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
                                     Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 180 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASGPGGGAPR 10
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                    US-09-165-546D-15
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RESULT 5
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECHONE: 617-720-3500
TELEPHONE: 617-720-3500
                  600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.5%;
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90.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                        COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASGPGGGAPR 10
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US-09-341-829A-5
                                       Boston
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US-09-341-829A-5
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LENGTH: 210
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GENERAL TABLE APPLICANT: Leth, Charles

APPLICANT: Lucas, Sophie

APPLICANT: Lucas, Sophie

APPLICANT: De Smet, Charles

APPLICANT: Good-laine, Daniele

APPLICANT: Good-laine, Daniele

TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS

TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS

CURRENT APPLICATION NUMBER: US/09/341,829A

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: PCT/US98/01445

NUMBER OF SEQ ID NOS: 14

SEQ ID NOS: 14

SEQ ID NOS: 14

SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                              85.5%; Score 47; DB 1; Length 180; 90.0%; Pred. No. 30; tive 0; Mismatches 1; Indels
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Sequence 5, Application US/08791495

Patent No. 5811519

GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 90.0
Matches 9; Conservative
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53 ASGPRGGAPR 62
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-341-829A-7
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gequence 5, Application US/09341829A

patent No. 6794131

GENERAL INFORMATION:
APPLICANT: Lucth,, Bernard
APPLICANT: Luch, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A

CURRENT PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: BC7/US98/01445

PRIOR APPLICATION NUMBER: PCT/US98/01445

SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 2; Length 210;
Pred. No. 34;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 1; Length 210;
Pred. No. 34;
0; Mismatches 1; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
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Sequence 24933, Application US/09252991A

Fatent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 10196-123
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
FRIOR FILING DATE: 1998-07-27
FRIOR FILING DATE: 1998-07-27
FRIOR PARTOR FILING DATE: 1998-07-27
APPLICANT: Pfreundschuh, Michael
TILE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039A
CURRENT TLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR PILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR PLING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR PLING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR APPLICATION NUMBER: US 09/105,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2; Length 9;
Pred. No. 4.6e+05;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.2%;
80.0%;
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Best Local Similarity 100.
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASGPGGGA 8
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US-09-252-991A-24923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 107196_136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: US 60/094,190

NUMBER: US 60/094,190

NUMBER: US 60/094,190

SEQ ID NOS: 33142

SEQ ID NOS: 33142
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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                Sequence 32326, Application US/09252991A Patent No. 6551795
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; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative 0
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Matches 8; Conservative
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US-09-344-040C-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASGPGGGAP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-32326
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US-09-833-039A-117
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27, Appl 1454, Ap 188, App 388, App 69, Appl 75, Appl 75, Appl 75, Appl 75, Appl 75, Appl 75, Appl 76, Appl 77, Appl 76, Appl 76, Appl 77, Appl 76, Appl 76, Appl 76, Appl 77, Appl 76, Appl 76, Appl 77, Appl 76, Appl 76, Appl 77, Appl 76, Appl 77, Appl 76, Appl 76, Appl 77, Appl 77,

Scoring table:

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US-10-296-734-1454

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US-10-188-812-141

US-10-117-937-75

US-10-117-937-75

US-10-10-734-834

US-10-657-022-75

US-10-657-022-75

US-11-067-05-75

US-11-067-03-76

US-11-067-037-76

US-11-157-031-88

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APPLICANT: Tafuro, Sabrina
APPLICANT: Medichael, Andrew James
APPLICANT: McMichael, Andrew James
APPLICANT: Bell, John Irving
APPLICANT: Hauter, Michael
ITILE OF INVENTION: Cancer Therapy
ITILE REFERENCE: 3547.1001-000
CURRENT APPLICATION NUMBER: US/10/415,841A
CURRENT FILING DATE: 2004-01-21
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASELSEQ for Mindows Version 4.0
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; Sequence 52, Application US/10415841A
; Publication No. US20040131598A1
; GENERAL INFORMATION:
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Matches 10; Conservative
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                                                                                                                                                                                        March 13, 2006, 19:51:56 ; Search time 60.4706 Seconds (without alignments) 69.096 Million cell updates/sec
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Sequence 13,
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'cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-128-506A-23

US-10-296-734-1404

US-10-482-029-202

US-09-751-798-8

US-09-751-798-8

US-10-027-655-71

US-10-026-06-3

US-10-026-06-3

US-10-137-74

US-10-296-734-832

US-10-188-15-11

US-10-175-088-15

US-10-657-022-74

US-10-877-37-31

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Patent No. US20020010321A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chuth, Alexander; Old, Inloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 5; Length 179; 100.0%; Pred. No. 7.8;
                                                              100.0%; Score 55; DB 4; Length 30; 100.0%; Pred. No. 1.6;
                                                                                                                 0; Indels
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage compuTER: IBM
                                                                                                                                                                                                                                                                                                              Sequence 202, Application US/10482029
Publication No. US20050037445A1
GENERAL INFORMATION:
APPLICANT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REPREBREE: P 573 PC00
CURRENT APPLICATION UNMER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Patentin version 3.1
SEQ ID NO 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 1010.
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APPLICATION NUMBER: US/09/751,798
; OTHER INFORMATION: NYSOla segment 4 US-10-296-734-1404
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APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-482-029-202
                                                                                                                                                                                                                                                                            RESULT 5
US-10-482-029-202
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Sequence 23, Application US/10182506A

Febblication No. US20550136402A1

Sequence 23, Application US/10182506A

Febblicant No. US20550136402A1

GENERAL INFORMATION:

APPLICANT: Rosenberg, S A

APPLICANT: Zeng, G

TITLE OF INVENTION: ANTIGEN, NY ESO-1

TITLE OF INVENTION: ANTIGEN, NY ESO-1

FILE REPERENCE: 21952

CURRENT APPLICATION NUMBER: US/10/182,506A

CURRENT APPLICATION NUMBER: US/10/182,506A

CURRENT APPLICATION NUMBER: 60/179,004

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/179,004

PRIOR APPLICATION NUMBER: 60/179,004

PRIOR APPLICATION NUMBER: 60/237,107

PRIOR PLING DATE: 2000-09-29

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 10
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Publication No. US20040054137A1

GENERAL INPORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

PRIOR APPLICATION NUMBER: US/10/296,734

PRIOR RILING DATE: 2003-08-04

PRIOR RILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 1404

LENGTH: 30
                                                                                                                                  Query Match 100.0%; Score 55; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 0.61; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 5; Length 10; 100.0%; Pred. No. 0.61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-10-182-506A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
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US-10-296-734-1404
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SEQ ID NO 52
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Sequence 71, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
FILLE OF INVENTION: BINDION DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILLE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 4; Length 180; 100.0%; Pred. No. 7.9;
      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. US20020164665Alman D. REGIGFRATION UNDRER: 30,946
REPERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                              OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                          APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: COMMERS: 08/725,182
FILING DATE: OCCOBER 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 318-3168 (ELEFAX: (212) 752-5958
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US-10-364-614-14
; Sequence 14, Application US/10364614
; Septence 14, Application US/2550A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-teeng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE BERERNCE: L0461/7105 (RW)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
               NAME: Hanson, No. US20020010321Alman D. REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 316-3168
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Sequence 30, Application US/09849602
Publication No. US20030165834A1
                                                                                                       TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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STATE: New York
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           10; Conservative
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: Macray, Richard
APPLICANT: Matray, Richard
APPLICANT: Wateson, Susan R.
APPLICANT: Wateson, Susan R.
APPLICANT: Wateson, Susan R.
APPLICANT: Wateson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-12
PRIOR PILING DATE: 2001-11-12
PRIOR PILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2002-11-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 2002-01-00
PRIOR PILI
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            APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR PELLING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR PLING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FRSESEQ for Windows Version 4.0
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
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CORGANISM: Homo sapiens
US-10-117-937-74
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US-10-295-027-386
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APPLICANT: KNUTH, Alexander
APPLICANT: OLD Lloyd
APPLICANT: OLD Lloyd
APPLICANT: Gnjatic, Sacda
APPLICANT: Gnjatic, Sacda
TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
FILE REFERENCE: LUD 5726.1 CIP
CURRENT PAPLICATION NUMBER: US,10/364,614
CURRENT FILING DATE: 2003-02-24
PRIOR PILING DATE: 2003-02-24
PRIOR PLILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 14
LENGTH: 180
TYPE: PRT
CREANT: Home sapiens
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| Publication No. US20030215425A1
| GENERAL INFORMATION:
| APPLICANT: Sinard, John J. L. |
| APPLICANT: Diamond, David C. |
| TITLE OF INVENTION: PRESENTING CELLS |
| FILE REFERENCE: CTLIAM. 21CPLC |
| CURRENT APPLICATION NUMBER: US/10/026,066 |
| CURRENT PILING DATE: 2000-04-28 |
| PRIOR PELING DATE: 2000-04-28 |
| PRIOR PLING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-026-066-3
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GENERAL INFURMATION:
APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
APPLICANT: Baiz, Natasha
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE REFERENCE: 018501-002300S
TITLE REFERENCE: 018501-002300S
CURRENT APPLICATION NUMBER: US 60/310,099
PRIOR PILING DATE: 2001-00-03
PRIOR PELING DATE: 2001-10-03
PRIOR PELING DATE: 2001-11-08
PRIOR PELING DATE: 2001-11-10
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR PELING DATE: 2001-11-13
PRIOR SEQ ID NOS: 207
SOFTWARE: PATENTIN UNBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SEQ ID NO 139
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                                                                                                                                                                                              Gaps
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                                                                                                                                 Query Match 100.0%; Score 55; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 7.9; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REPERSOR: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR PILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin version 3.2
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 55; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 7.9; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                           0; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: NYNSOla consensus polypeptide US-10-296-734-832
                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 832, Application US/10296734 Publication No. US20040054137A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 139, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                          1 ASGPGGGAPR 10
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; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT 'CORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-10-296-734-832
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; LENGTH: 180
; TYPES PRT
; CRGANISM: Homo sapiens
US-10-188-832-139
Query Match

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62
Search completed: March 13, 2006, 20:02:26
Job time: 60.4706 secs
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RESULT 2
US-11-021-441-28
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\begin{array}{c} \mathbf{n} \\ \mathbf{
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Sequence 28, Appl
Sequence 3169, App
Sequence 3169, Appl
Sequence 3295, Appl
Sequence 7762, Appl
Sequence 2722, Appl
Sequence 8, Appl
Sequence 9, Appli
Sequence 18, Appl
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Sequence 22845, A
Sequence 22805, A
Sequence 20556, A
Sequence 988, Appli
Sequence 9, Appli
Sequence 21887, A
Sequence 21887, A
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                             March 13, 2006, 19:54:06; Search time 6.82353 Seconds (without alignments) 40.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, A
Sequence 18, A
Sequence 63, A
Sequence 18, A
Sequence 184,
Sequence 16457
Sequence 22845
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-021-41-28
US-10-072-512-3369
US-11-072-512-3369
US-11-072-512-3265
US-11-087-099-7762
US-11-087-099-7762
US-11-087-099-7762
US-11-240-765-58
US-10-992-577-8
US-10-992-577-8
US-11-078-735-18
US-11-078-735-18
US-11-078-735-18
US-11-096-568A-16457
US-11-096-568A-22645
US-11-096-568A-22645
US-11-096-568A-22645
US-11-096-568A-22645
US-11-096-568A-22645
US-11-096-568A-20656
US-11-096-568A-20656
US-11-096-568A-20656
US-11-096-568A-20656
US-11-096-568A-20656
US-11-096-568A-20656
US-11-096-568A-20699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161667 seqs, 27834885 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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55
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Match Length DB
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                                                                                                                                                                                                                                                                                                                    Perfect score:
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                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                                                   Run on:
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No.
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26 37 67.3 198 7 US-11-096-568A-22493 Sequence 22494, A 28 37 67.3 269 7 US-11-096-568A-22493 Sequence 22493, A 28 37 67.3 401 7 US-11-096-568A-381 Sequence 16, Appl 30 37 67.3 401 7 US-11-096-568A-381 Sequence 382, Appl 31 37 67.3 401 7 US-11-096-568A-383 Sequence 381, Appl 31 37 67.3 1465 7 US-11-096-568A-381 Sequence 381, Appl 32 37 67.3 1465 7 US-11-087-099-1095 Sequence 1792, Appl 33 37 67.3 1465 7 US-11-087-099-1059 Sequence 1059, Appl 34 37 67.3 2923 7 US-11-087-099-1059 Sequence 1059, Appl 36 56.4 167 7 US-11-200-822-3 Sequence 1059, Appl 36 55 66.4 190 7 US-11-143-568A-1910 Sequence 21910, Appl 36 65.5 155 7 US-11-143-586-3 Sequence 15, Appl 40 36 65.5 107 7 US-11-14-325-15 Sequence 15, Appl 41 36 65.5 188 6 US-10-821-34-941 Sequence 19104, Appl 44 36 65.5 238 7 US-11-194-890-15 Sequence 10553, Appl 44 36 65.5 238 7 US-11-194-890-15 Sequence 10553, Appl 44 36 65.5 238 7 US-11-194-890-15 Sequence 10553, Appl 44 36 65.5 238 7 US-11-194-890-15
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ALIGNMENTS

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RESULT 2

US-11-155-288-7

US-11-155-288-7

Sequence 7, Application US/11155288

PUBLICANT: Chiang, Chih. Sheag

APPLICANT: Chiang, Chih. Sheag

APPLICANT: Chiang, Chih. Sheag

APPLICANT: Chiang, Chih. Sheag

TITLE OF INVENTION: CHORENATION: CHORENATIO
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Score 41; DB 7; Length 555; Pred. No. 76; 1; Mismatches 1; Indels
                                                                                                                                                                         APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/11037243; Publication No. US20050287546A1; GENERAL INFORMATION:
                                                                                          TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAGAI, KEIICHI
IRIE, RYOTARO
                                 OTSUKA, KAORU
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-072-512-3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASGPGGGAP 9
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US-11-072-512-3295
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LENGTH: 953
                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-10-623-155-496

Sequence 496, Application US/10623155

Sequence 496, Application US/10623155

SHUDIcation No. US20050261166A1

GENERAL INFORMATION:

APPLICANT: Wange, Tongtong

APPLICANT: Retter, Marc W.

APPLICANT: Panger, Gary R.

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND INFORMATION INMERR: US/10/623,155

CURRENT PILLING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SEQ ID NO 496

LENGTH: 20

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 55; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-08-05
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-06-30
PRIOR PRILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.2%; Score 43; DB 100.0%; Pred. No. 2.4 tive 0; Mismatches
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Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: SUGITYAMA, TOMOYASU
APPLICANT: SUGITYAMA, TOMOYASU
APPLICANT: STATO, HISTOUI
APPLICANT: SATO, HISTOUKI
APPLICANT: SATO, HISTOUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII SHIZUKO
APPLICANT: ISHII SHIZUKO
APPLICANT: ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
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13 ASGPGGGA 20
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US-11-072-512-3369
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Gaps

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0
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GENERAL INFOGRATION
APPLICANT: WHYTE, DAVID
APPLICANT: GARIEPEEL, SEAN
APPLICANT: CAREPEEL, SEAN
APPLICANT: CHARYDEEL, SEAN
APPLICANT: CHARYDEEL, SEAN
APPLICANT: CHARYDEEL, SEAN
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, SERARD
CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTIN VET. 2.1
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Score 39; DB 7; Length 213; ; Pred. No. 63;
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JAPPLICATT: SOPPET et al.

TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REPERENCE: PZ037PLC2

CURRENT APPLICATION NUMBER: 09/997,131

PRIOR APPLICATION NUMBER: 09/997,131

PRIOR APPLICATION NUMBER: 09/997,131

PRIOR FILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-68

PRIOR PILING DATE: 1999-02-10

PRIOR PILING DATE: 1999-02-10

NUMBER OF SEQ ID NOS: 173

SOFTWARE: PACHILIN Ver: 2.0

SEQ ID NO 58

LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%; bcc.
100.0%; Pred. No. c...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2722
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OFSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVel full length cDNA
                         Sequence 2722, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-11-240-769-58
Squence 58, Application US/11240769; Publication No. US20060036089A1; GENERAL INFORMATION:
                                                                                      APPLICANT: 1SOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                               NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                             OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2722
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ORGANISM: Homo sapiens
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Matches
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Pred. No. 2.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.7%; Score 40; DB 7; Length 678; 77.8%; Pred. No. 1.2e+02; tive 1; Mismatches 1; Indels
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Publication No. US20060041961A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B.P.
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7762
                                                                                                                                                                                                                                                                             APPLICANT: NAGAL, KELICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: SEKL, INDAHKO
APPLICANT: SEKL, INDAHKO
APPLICANT: SEKL, INDAHKO
APPLICANT: SOSUKAWA, TSTTOMU
APPLICANT: YOSHIKAWA, TSTTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERRNCE: 084335-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE PATENTIN VEY: 2.1
SOFTWARE PATENTIN VEY: 2.1
Sequence 3295, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                             APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZOKO
APPLICANT: ISHII, SHIZOKO
APPLICANT: ISONO, YUUKO
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77.8%;
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; ORGANISM: Podospora anserina
US-11-087-099-7762
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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OTSUKA, KAORU
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1051 SGSGGSPR 1059
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US-11-072-512-3295
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APPLICANT:
APPLICANT:
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Gaps

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Indels

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) ORGANISM: Human
US-11-223-294-54
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US-11-078-735-18
                   LENGTH: 430
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US-10-508-892-2
Sequence 2, Application US/10508892
Sequence 2, Application No. US20060014218A1
GENERAL INFORMATION:
APPLICANT: Golz, Stefan
APPLICANT: Weingartner, Bernhard
APPLICANT: Weingartner, Bernhard
TITLE OF INVENTION: Neuropeptics and Therapeutics for Diseases Associated with
TITLE OF INVENTION: Neuropeptics and Therapeutics for Diseases Associated with
FILE REPERSUCE: Le A 35 944
CURRENT APPLICATION NUMBER: PO14-09-22
PRIOR APPLICATION NUMBER: PO14-09-22
PRIOR APPLICATION NUMBER: PO2006654.4
FRIOR APPLICATION NUMBER: EP 02006654.4
FRIOR PILING DATE: 2003-03-14
FRIOR PILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10992577
Publication No. US20050260687A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gores, Kenneth A.
APPLICANT: Borowsky, Beth B.
ITLE OF INVENTION: Douglas A.
ITLE OF INVENTION: DAM Encoding Mammalian Neuropeptide FF (NPFF) Receptors
ITLE OF INVENTION: DAM Encoding Mammalian Neuropeptide FF (NPFF) Receptors
ITLE OF INVENTION: DAM USES Thereof
FILE REFERENCE: 57155-D/JFW
CURRENT APPLICATION NUMBER: US/10/992,577
CURRENT APPLICATION NUMBER: US/09/538,036
PRIOR PILING DATE: 1999-09-24
PRIOR PILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 71
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; LOCATION: (168); COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-11-240-769-58
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                       Query Match 70.9%; Score 39; DB 7; Length 233; Best Local Similarity 87.5%; Pred. No. 68; Matches 7; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 77.8
Matches 7; Conservative
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LENGTH: 430
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Publication No. US2005026147741

GENERAL INFORMATION:

APPLICANT: CHAMPION, BRIAN ROBERT

APPLICANT: CHAMPION, BRIAN ROBERT

APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: TUGAL, TAMARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS

TITLE OF INVENTION: COMPRISING NOTCH LICAND PROTEINS

TITLE OF INVENTION: COMPRISING NOTCH LICAND PROTEINS

TITLE OF INVENTION: COMPOSITION NOTCH LICAND PROTEINS

TILLE REFERENCE: 674525-2019

CURRENT PILING DATE: 2005-09-09

PRIOR APPLICATION NUMBER: PCT/GB03/03908

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-04

PRIOR PILING DATE: 2003-09-04

PRIOR PILING DATE: 2003-09-04

PRIOR PILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: PCT/GB03/01525

PRIOR PILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: PCT/GB03/0534.2
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77.8%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                      2; Indels
                                                                      Score 39; DB 6;
Pred. No. 1.1e+02;
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WESULY 12

SEQUENCE 54, Application US/11223294

SEQUENCE 54, Application US/11223294

SEQUENCE 54, Application US/11223294

SEQUENCE 54, WESULY US/11223294

APPLICANT: YOSHIDA, Hiromi
APPLICANT: YOSHIDA, Hiromi
APPLICANT: HABATA, YUGO

TITLE OF INVENTION: NOVEL RFRP-3 And Its DNA
FILE REFRENCE: 2944USOP

CURRENT APPLICATION NUMBER: US/11/223,294

CURRENT APPLICATION NUMBER: US/10/487,634

PRIOR APPLICATION NUMBER: PCT/JP02/08466

PRIOR APPLICATION NUMBER: PCT/JP02/08466

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2005-09-09

PRIOR FILING DATE: 2005-09-09

NUMBER OF SEQ ID NOS: 78

LENGTH: 430
                                                                                                                      0; Mismatches
                                                                      70.98;
                                                    Query Match
Best Local Similarity 77.0
Best Tocal 7; Conservative
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ORGANISM: Homo sapiens
US-10-508-892-2
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APPLICANT: GHAMPION, BRIAN ROBERT

APPLICANT: CHAMPION, BRIAN ROBERT

APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: LENNARD, ANDREW CHRISTOPHER

APPLICANT: WARD, GRANGE ALBERT

TITLE OF INVENTION: GENCE ALBERT

TITLE OF INVENTION: GENCE ALBERT

TITLE OF INVENTION: THEIR USE IN MEDICAL TREATMENT

FILE REFERENCE: 6745.25-20.3

PRIOR APPLICATION NUMBER: US/11/050,346

CURRENT APPLICATION NUMBER: BD 0312062.3

PRIOR FILLING DATE: 2003-05-24

PRIOR FILLING DATE: 2003-04-04

PRIOR FILLING DATE: 2003-04-04

PRIOR FILLING DATE: 2002-09-07

PRIOR APPLICATION NUMBER: GB 0320849.4

PRIOR FILLING DATE: 2002-09-07

PRIOR FILLING DATE: 2002-09-10

PRIOR FILLING DATE: 2002-09-10

PRIOR FILLING DATE: 2002-11-13

PRIOR FILLING DATE: 2002-11-13
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PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/GB02/05133
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-09-10
PRIOR FILING DATE: 2002-09-10
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTIN VET. 3.3
SEQ ID NO 18
LENGTH: 618
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; Sequence 63, Application US/11050346
; Publication No. US20060002924A1
; GENERAL INFORMATION:
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US-11-078-735-18
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; ORGANISM: Homo sapiens
US-11-050-346-63
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RESULT 15

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WESULT 15

SEQUENCE 18, Application US/11103077

PUBlication No. US2066003927A1

GENERAL INFORMATION:

PUBLICANT: GHANGLEE LYNN

TITLE OF INVENTION: MODILATION OF IMMUNE FUNCTION

FILE REFREENCE: 67452-674-11

FILE REFREENCE: 67452-674-11

FRICA APPLICATION NUMBER: US/11/103,077

CURRENT APPLICATION NUMBER: CB 0223405.2

PRIOR PILING DATE: 2003-10-09

PRIOR FILING DATE: 2002-10-09

PRIOR FILING DATE: 2003-30-09

PRIOR FILING DATE: 2003-30-
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                                                                                                                 March 13, 2006, 18:52:59 ; Search time 112.941 Seconds (without alignments) 58.355 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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geneseqp2003as:*
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay05978 Human can	Aay05979 Human can	Aau85105 Human NYN	Epitop	Aaw62584 Cancer as	Aaw69665 Human NY-	Aay05965 Human can	Aay52430 Human tum	Aay70862 Human tum	Aab03154 Human oes	Aab69946 Human NY-	Aag67164 Amino aci	Aau01535 Human NY-	Aae07714 Human NY	Aau84818 Human NYN	6	Abr58672 Human can	Abr48210 Human bla	Abu56508 Lung canc	Abu56694 Lung canc	Abp74198 Human NY-	Abu64816 Human NY-	Abr83438 Human NY-	Adc09576 NY-ESO-1
SUMMARIES	at	AAY05978	AAY05979	AAU85105	ADK68648	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164	AAU01535	AAE07714	AAU84818	AAU11543	ABR58672	ABR48210	ABU56508	ABU56694	ABP74198	ABU64816	ABR83438	ADC09576
	DB	7	7	Ŋ	æ	7	~	~	ო	ო	ო	4	4	4	4	S	Ŋ	9	9	9	9	9	9	9	7
	% Query Match Length	15	20	30	179	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180
d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78
	Result No.		7	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

	Add35568 Human NY-		Adj54139 Human NY-	Adm72815 Human NY-	Adm73418 CAG-3 pro	Human	Adq18451 Human sof	Adq10446 Autoimmun	Ads80926 Tumour as	Adw44353 Human aut	Ady85096 Tumor ant	Adz28913 NY-ESO-1	Adz42374 Immunogen	Aea35651 Human NY-	Adw99402 NY-ESO-1/	Aeb80047 Human NY-	Aae13122 NY-ESO-IC	Aau85130 Human mel	Aay05986 Human can
7 ADD35564	7 ADD35568	7 ADN39068	8 ADJ54139	8 ADM72815	8 ADM73418	8 ADM73417	8 ADQ18451	8 ADQ10446	8 ADS80926	9 ADW44353	9 ADY85096	9 ADZ28913	9 ADZ42374	9 AEA35651	9 ADW99402	9 AEB80047	4 AAE13122	5 AAU85130	2 AAY05986
180	0 0	180	180	180	180	180	180	180	180	180	180	180	180	180	240	240	397	3541	14
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.9
78	20 00	7 0	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	74
25	9 6	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAX05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAX05966), portions of them and their variants (see AAX05967-81), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kichey cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide. (USSH) US DEPT HEALTH & HUMAN SERVICES. AAY05978 standard; peptide; 15 AA. Claim 15; Page 64; 88pp; English. Cancer antigen NY ESO1/CAG-3. 97US-0061428P. 98WO-US019609 (first entry) Wang RF, Rosenberg SA; WPI; 1999-277270/23. WO9918206-A2. 21-SEP-1998; Homo sapiens 08-OCT-1997; 15-APR-1999. vaccine. AAY05978

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cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, estrical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
      the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
                                                                                                                                                                                                                                                                                    return to a patient
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Sequence 15 AA;

Gaps ö Score 78; DB 2; Length 15; Pred. No. 0.0029; ; Mismatches 0; Indels 0; Mismatches 100.08; 100.08; 1 AGAARASGPGGGAPR 15 1 AGAARASGPGGGAPR 15 15; Conservative Query Match Best Local Similarity Matches ð

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AAY05979 standard; peptide; 20 AA. (first entry) 16-AUG-1999 RESULT 2

Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine,

sapiens. Synthetic

WO9918206-A2

15-APR-1999

21-SEP-1998;

97US-0061428P 08-OCT-1997; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Rosenberg SA; Wang RF,

WPI; 1999-277270/23.

Cancer antigen NY ESO1/CAG-3.

Claim 16; Page 64; 88pp; English.

The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05955), as new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an

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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked cogether in a different relativoship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypucides needing and computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides synthetic polypeptides. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas prostate, stomach, bladder, kidney, bone liver, one pophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one parent polypeptide linked together differently compared to the
linkage in the parent polypeptide, for inducing immune response against a
                 cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New synthetic polypeptides having several different segments of at least
                                                                                                                                                                                                                                                 Gaps
HLA molecule. The cancer peptides form part of, or are derived from,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection;
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                                                                                                                                                                                                        100.0%; Score 78; DB 2; Length 20; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU85105 standard; peptide; 30 AA
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                                                                                                                                                                                                                                Sest Local Similarity
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                                                                                                                                                                 Sequence 20 AA;
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                                                                                                                                                                                                             Query Match
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where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine development or in the generation or expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunocherapy. The invention is also useful for activating T-cells against neoplastic cells, and cells infected with virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing target cells in the host. The present sequence is that of a protein which is related to the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer associated antigen; NY-ESO-1; regression; progression; onset;
                                                                                                                                                                                                                                                      100.0%; Score 78; DB 8; Length 179; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer associated antigen NY-ESO-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; treatment; diagnosis.
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                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                         1 AGAARASGPGGGAPR
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                                                                                                                                                                                                                        Sequence 179 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proceasome; contacting the aubstrate with a composition including the proteasome, under conditions that support processing of the substrate by proteasome; and assaying for liberation of epitope. The invention may be useful for protozoacide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation,
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the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitope liberation; substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekkeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Bstein-Barr virus and respiratory synocytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophlus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence a peptide derived from a parent protein used to construct a savine of
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                                                                                                                                                                                       Length 30;
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                                                                                                                                                                                       Score 78; DB 5;
Pred. No. 0.0054;
                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        ADK68648 standard; protein; 179 AA.
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                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                        1 AGAARASGPGGGAPR 15
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DIAMOND D C.
QIU Z.
LEI X.
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                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                      Sequence 30 AA;
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                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                           ADK68648;
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(DIAM/)
(QIUZ/)
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Knuth A;

ö The present sequence represents human NY-ESO-1, formerly known as IL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to a meeliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, containing monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, Gaps Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour. Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone. ; Godelaine D, Boon-Falleur T; Score 78; DB 2; Length 180; Pred. No. 0.027; Mismatches 0; Indels Example 2; Page 57-58; 73pp; English AAW69665 standard; protein; 180 AA. . (LUDW-) LUDWIG INST CANCER RES. De Smet C, 100.0%; 98WO-US001445 97US-00791495 48 AGAARASGPGGGAPR 62 (first entry) Query Match Best Local Similarity 100. Matches 15; Conservative tumours. WPI; 1998-427951/36. Lucas S, therapeutic regime Sequence 180 AA; N-PSDB; AAV50348 Homo sapiens. WO9832855-A1. 27-JAN-1998; 27-JAN-1997; particularly 27-0CT-1998 30-JUL-1998 AAW69665; Lethe B, **AAW69665** ¥8888888888888 g CCCCCCCCCCCCX8X444X84X1X8X8X6X6X6X6X8X8X8X8X6X6CCC

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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and concerned to the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and concerned to the periods of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see CAMY05966), portions of these peptides and their variants (see AAY05965-CAMY05966), portions of these peptides and their variants (see AAY05965-CCAMY05966), portions of these peptides that protect the recipient from a ransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with the CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide. Or with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, cervical cancer, bladder cancer, leukaemia, uterine cancer, lymphoma, sarcoma, lung cancer, lidney cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; shidney cancer; pancreatic cancer; liver cancer; sarcoma;
                        enrich
T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrethe isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                             100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAY05965 standard; protein; 180 AA.
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                                                                                                                                                                                                                                         15; Conservative
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N-PSDB; AAX58599.
                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                         Sequence 180 AA;
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AAY05965
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This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and cumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY -ESO-1 are bound by both MRC (major histocompatibility complex) Class I and class I molecules for presentation to T-cells. Peptides AAV52431- V52434 bind to class I HIA-A2 molecules, thereby stimulating place and class II HIA-DES molecules, stimulating helper T-cell proliferation. The poptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, prostate cancer, or lymphoma) and to stimulate the proliferation of T cells
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s= "Peptide presented by MHC Class I HLA-A24 and HLA-
                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Peptide (AAY52434) presented by MHC Class I HLA-
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                                                                                                                                                   /note= "Peptide presented by MHC Class I HLA-A24"
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%= "Peptide presented by MHC Class I HLA-A3"
                                                  'note= "Peptide presented by MHC Class I HLA-A3"
                                                                                                                                                                                      "Peptide presented by MHC Class I HLA-B8"
                                                                                                                                                                                                                     /note= "Peptide presented by MHC Class I HLA-B7"
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                     "Peptide presented by MHC Class I HLA-B7"
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                                                                                  presented by MHC Class
                                                                  118. .126 /
/note= "Peptide
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98US-00165546.
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                     'note=
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Gure A, Ritter G;
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//note= "Peptide presented by MHC Class I HLA-B52"
113. .122
/note= "Peptide presented by MHC Class I HLA-B52"
Anote= "Peptide presented by MHC Class I HLA-B7 and HLA-B52"
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                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytocoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                     Gaps
treated by inducing cancer-specific T cells in vitro for subsequent return to a patient
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:e= "Peptide presented by MHC Class I HLA-B44"
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.e= "Peptide presented by MHC Class I HLA-B7"
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== "Peptide presented by MHC Class I HLA-B7"
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e= "Peptide presented by MHC Class I HLA-B7"
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/note= "Peptide presented by MHC Class I HLA-A1"
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                                                                                100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                   AAY52430 standard; protein; 180 AA.
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/note= "Peptide
                                                                                                                                                                                                                                                                                                                                                                                      Human tumour antigen NY-ESO-1.
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(first entry)
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                                                                           Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .108
                                                                                                                                                                               48 AGAARASGPGGGAPR
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                                                 Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Unidentified
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15-PEB-2000
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AAB03154 standard; protein; 180 AA.

RESULT 10

AAB03154

AAB03154;

48 AGAARASGPGGGAPR 62

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                                                                                                                                                                                                                                                                                                                                                                                                  NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
               Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                   Gaps
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                                                                                 Length 180;
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                                                                               Score 78; DB 3;
Pred. No. 0.027;
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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N-PSDB; AAD00152.
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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a cDNA library prepared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, everal n-myristoylation sites and o-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The antigen is useful as an immunogen when combined with an adjuvant, in both precursor and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions,
                                                                                                                    Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                  note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                    note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                               note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                              /note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Potential transmembrane domain"
                                                                                   Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Y, Tureci O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 3; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00013150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00725381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. infections and cancer.
                                                  23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-410880/35.
N-PSDB; AAA61483.
                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-1996;
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6069233-A.
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Gaps

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Query Match 100.0%; Score 78; DB 3; Length 180; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 15; Condervative 0; Mismatches 0; Indels

1 AGAARASGPGGGAPR 15

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Query Match
                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing or remaining stable, in particular in patients receiving treatment for a method is a denocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.
targetted delivery of therapeutic agents to oesophageal cancer cells. It can also be used to generate diagnostic or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                            Human, NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scanlan M;
                                                                                       Score 78; DB 3; Length 180;
Pred. No. 0.027;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                  AAB69946 standard; protein; 180 AA.
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                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-2000; 2000WO-US019220.
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                                                                                                                                                           1 AGAARASGPGGGAPR 15
                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                            48 AGAARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                         Human NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-182822/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF58634.
                                                   Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200107917-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carcinoma
                                                                                                                                                                                                                                                                                                                     AAB69946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jager E,
                                                                                                                                                                                                                                               RESULT 11
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NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; human leukocyte antigen-determining region; disease progression;
                                                                                                                                                                                                                                                                                                                                                                                        Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful for diagnosing testicular tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 78; DB 4; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NY-ESO-1 tumour rejection antigen precursor protein.
                                                                                                                                                                                AAG67164 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01535 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Fig 3; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-2001; 2001WO-US002126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2000; 2000US-00510635.
1 AGAARASGPGGGAPR 15
                                            AGAARASGPGGGAPR 62
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                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 180 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                     AAG67164;
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Gaps

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Query Match 100.0%; Score 78; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 15; Conservative 0; Mismatches 0; Indels

us-09-529-206e-26.rag

Human, major histocompatibility complex; MHC; vaccine; metastasis; cases II restricted T cell epitope; MHC-II epitope; cancer antigen; NY BSO-I protein; CD4 T lymphocyte; human leucocyte antigen; tumour-specific humoral-mediated immunity; cancer; cytostatic;

(first entry)

06-NOV-2001

AAE07714;

Human NY ESO-1 protein

45. .47 /note= "Encoded by CCCGGGGC"

Location/Qualifiers

Misc-difference

immunotherapy

Homo sapiens

WO200155393-A2

02-AUG-2001

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The sequence represents a human NY-ESO-1 tumour rejection antigen precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigen-determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC class II HLA-DR NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onserving the labelled or enzyme labelled monoclonal antibody which specifically binds with the complex
disease regression, disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78; DB 4; Length 180; Pred. No. 0.027;
                                                                                                                                                                                                                                                    /note= "Phosphorylated"
138
                                                                                                                                                                                     'note= "Phosphorylated"
                                                                                                                                                                                                                       'note= "Phosphorylated"
                                                                                                                                                                                                                                                                                         /note= "Phosphorylated"
                                                                                                                     'note= "Myristoylated"
                                                                                                                                                    "Myristoylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfreundschuh M;
                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00408036.
                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000; 2000WO-US026411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                     note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS02254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                           WO200123560-A2
                                                                                                  Modified-site
                                                                                                                                     Modified-site
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                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                       Modified-site
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                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tureci O,
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New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.

Example 1; Fig 1; 134pp; English.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

26-JAN-2001; 2001WO-US002765. 28-JAN-2000; 2000US-0179004P. 29-SEP-2000; 2000US-0237107P. ö

Rosenberg SA,

Wang R,

N-PSDB; AAD14179, AAD14180.

WPI; 2001-496851/54.

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NT ESO-I The MHC-II epitopes (TC mon NV ESO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR creatricted. The products of the gene are promising candidates for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection agent to detect the presence of cancer, to enhance useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 0.027;
Mismatches 0; Indels
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Gaps

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0; Indels

Mismatches

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1 AGAARASGPGGGAPR 15

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62

48 AGAARASGPGGGAPR

AAE07714 standard; protein; 180 AA.

RESULT 14 AAE07714

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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides. The synthetic polypeptides and polymucleotides concer, colypeptides and polymucleotides are referred to as a Savine. The synthetic polypeptides and polymucleotides are referred to as a Savine. The synthetic polypeptides on a savine. The synthetic polypeptides on a cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus (such as infections caused by Neisseria, Meningococcal, Haemophilus, virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, virus, a consensus sequence for a parent protein used to design a savine of the invantion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                                                Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonnella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 27; 364pp; English.
                                                                                           Human NYNSOla consensus sequence.
                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001; 2001WO-AU000622.
                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000AU-00007761
                                                                                                                                                                                                                                                                                                                                                                                                                              (AUSU ) UNIV AUSTRALIAN NAT.
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomson SA, Ramshaw IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogen or cancer.
                                                                                                                                                                                                                                                                      WO200190197-A1
                                                                                                                                                                                                                                 Homo sapiens.
                                                      08-MAY-2002
                                                                                                                                                                                                                                                                                                            29-NOV-2001
                  AAU84818;
```

ó Gaps ö 100.0%; Score 78; DB 5; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.

Sequence 180 AA;

ò 셤 Search completed: March 13, 2006, 19:03:59 Job time: 113.941 secs

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us-09-529-206e-26.rpr

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24; Search time 17.8235 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-26

1 AGAARASGPGGGAPR 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR, 80:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	acclimation protei		hypothetical prote				11	Ca2+/calmodulin-de	homeotic protein e	5-carboxymethyl-2-	flagellar basal-bo	hypothetical prote	spidroin 2, dragli	dnaK-type molecula	myristylated alani	collagen alpha 1 c	histone H1-5 [vali	transforming prote		transcription acti	H+-transporting tw	c-Crk - chicken	myristylated alani	MAP kinase 3 (EC 2	insulinoma-associa	regulatory protein	probable infB - My		regulatory protein
	ID	T04476	T36115	S50754	T21096	T21095	E72464	T35694	JC1451	C48423	AE3526	AB3648	C84673	A44112	A36333	S08341	A36226	S51660	TVFV10	A44988	A47008	S04673	A49011	A39169	A48082	A42750	802165	B70694	F87103	A87431
	DB	5	~	~	~	7	7	0	7	7	0	7	~	~	~	N	7	Н	н	7	~	0	-	7	٦	7	~	N	~	~
	Length	82	222	351	995	692	220	1690	380	333	504	173	275	627	651	335	730	226	232	259	269	286	305	309	379	510	619	0	924	954
ا عد	Match	64.1	64.1	62.8	62.2	62.2	61.5		0	59.0		57.7	57.7	57.7	57.7	57.1	57.1	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4
	Score	50	20	49	•	48.5	48	48	47	46	46	45	45	45	45	44.5	44.5	44	44	44	44	44	44	44	44	44	44	44	44	44
+[::000	No.		8	3	4	S	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

A;Gene: SCOEDB:SCE15.12c C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);

ó

Gaps

ö

3; Indels

Length 222;

Score 50; DB 2; Pred. No. 11; 2; Mismatches

Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative

1 AGAARASGPGGGAP 14

adenylate cyclase	CREB-binding prote	heterogeneous nucl	hypothetical prote	Hypothetical Prote	hypothetical prote	DNA-invertase - Rh	hypothetical prote	hypothetical prote	hypothetical prote	jun-D protein - ra	hypothetical prote	Ca2+/calmodulin-de	transcription fact	conserved hypothet	membrane transport	
A41350	T13828	A44192	T36874	AE3136	G98151	842585	T32525	D70803	B72677	JC4051	S55626	S28184	A49642	E82766	T30220	
7	7	7	~	7	7	7	7	7	~	7	~	~	7	~	7	
1134	3190	328	185	189	189	213	260	280	307	341	349	377	420	431	437	
56.4	56.4	55.8	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	
44	44	43.5	43	43	43	43	43	43	43	43	43	43	43	43	43	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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C;Species: Hordeum vulgare (Darley)
C;Accession: Taylore (Darley)
C;Accession: Taylore (Darley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: Tud476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Flant Mol. Biol. 33, 1013-1023, 1997
Flant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRAM stability and localisation of the low temperature responsive barley gene
A;Reference number: 215367; MUID:97299834; PMID:9154983
A;Recession: T04476
A;Accession: T04476
A;Accession: T04476
A;Accession: T182 cPHI>
A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000099CE5A; EMBL:X97917; NID:g1418969; P
A;Cross-references: cv. Igri
C;Genetics:
A;Gene: blt14.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
S;Accession: T36115
A;Reference number: 221597
A;Accession: T36115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-22 <MUR>
A;Residues: 1-22 <MUR>
A;Cross-references: UNIPROT: Q9X887; UNIPARC: UP10000DB008; EMBL: AL049707; PIDN: CAB41281
A;Experimental Bource: strain A3(2)
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable oxidoreductase - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 2
Pred. No. 4.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.1%;
69.2%;
acclimation protein 2 - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAARASGPGGGAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 GAARGAGAGGOVP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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533 AGAPRVGGPGVQMGGAP 549
                                                                                                                                                                                                                                                                                                                                     1 AGAARASGPG---GGAP 14
A, Experimental source: clone F18H3
C, Genetics:
A, Gene: CESP: F18H3.3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| | : ||||: |
181 AGATRVARPGGGSDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1437 GSANGSGPEGSAPR 1450
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Best Local Similarity 64.34
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: SCOEDB:SC7C7.16c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: APE2360
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T21096
R;Coles, L.
R;Coles, L.
A;Reference number: Z19373
A;Accession: T21096
A;Reference number: Z19373
A;Accession: T21096
A;Reference number: Z19373
A;Accession: T21096
A;Reference number: Z19373
A;Residues: 1-566 <WIL>
A;Residues: 1-566 <WIL>
A;Residues: 1-566 <WIL>
A;Residues: UNIPROT:Q19581; UNIPARC:UPI0000079311; EMBL:Z50110; PIDN:CAA90446.1;
A;Constrimental source: Clone F18H3
C;Genetics: Clone F18H3
A;Gene: CESP: F18H3.3b
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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5;Species: Caenorhabditis elegans
6;Space: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
6;Accession: T21095
8;Coles, L.
8;Coles, L.
8;Accession: T21095
8;Accession: T21095
8;Accession: T21095
8;Accession: T21095
8;Accession: Data Library, UNIPARC:UPI0000079930; EMBL:Z50110; PIDN:CAA90444.1;Accessions-references: UNIPROT:Q19579; UNIPARC:UPI0000079930; EMBL:Z50110; PIDN:CAA90444.1;
                                                                                                                                                                     hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
E;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring, P. Hant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754
A;Accession: S50754
A;Accession: S50754
A;Accession: S50754
A;Accession: Jash WOBS
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2; Length 351;
Pred. No. 22;
2; Mismatches 3; Indels
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Best Local Similarity 64.3%;
Matches 9; Conservative
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180 SGSARASGPSAGRP 193
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295 SGSPRASPPGGGPP 308
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hypothetical protein APE2360 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72464
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takabawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; R
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyx
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Streptcomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35694
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: 221587
A;Accession: T35694
A;Accession: T35694
A;Accession: T35694
A;Accession: T3690 + ARA>
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1690 + ARA>
A;Residues: 1-1690 + ARA>
A;Escheres: UNIPROT: O86821; UNIPARC: UPI0000DACB6; EMBL: AL031031; PIDN: CAA19862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 «KAW»
A;Cross-references: UNIPROT:Q9Y9C7; UNIPARC:UPI000005E2F9; DDBJ:AP000064; NID:g5105945;
A;Experimental source: strain K1
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A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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0
                                                                                                                                               DB 2; Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 2; Length 1690;
Pred. No. 1.1e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Score 48; DB 2; Length 220; 60.0%; Pred. No. 20; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: Aeropyrum pernix hypothetical protein APE2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP dependent DNA helicase - Streptomyces coelicolor
                                                                                                                                    Query Match
62.2%; Score 48.5; D
Best Local Similarity 64.7%; Pred. No. 45;
Matches 11; Conservative 0; Mismatches
```

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R.DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8YDP0; UNIPARC:UP10000058376; GB:AE008918; PIDN:AAL53376.1
A;Experimental source: strain 16M
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A,Map postinon: II
C,Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C,Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                         5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (BC 1.2.1.-) [imported]
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                                                                                                                                                                                                                                                                                                                                                                   C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3526
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
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      Length 333
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Pred. No. 39;
0; Mismatches
ore 46; DB;
ed. No. 51;
Mismatches
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2; Mismatches
      Score 46;
Pred. No.
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Pred. No.
   59.0%;
64.3%;
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66.7%;
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Best Local Similarity 64.3%;
Matches 9; Conservative
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166 AGAAKAQGDGGETP 179
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                                                             Conservative
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Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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A;Cross-references: UNIPARC:UP100001707CE; GB:U12008; GB:S59509; NID:G515498; PIDN:AAA20
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin
F;41-331/Domain: protein kinase homology cKIN>
                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: P21708; UNIPARC: UPI000012F174; EMBL: X65198; NID: 956626; PIDN
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A; Residues: 14-380 <BOU>
A; Cross = references: UNIONO0145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID:
A; Cross = references: UNIONO A; J.S.; Cobb, M.H.
Biochemistry 30, 278-286, 1991
A; Title: Purification and properties of extracellular signal-regulated kinase 1, an insu
A; Reference number: A37140; MUID:91105092; PMID:1846291
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R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I.
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I.
A;Title: A;Title: Asquence comparison of the mouse, human, and chicken engrailed gene A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source: brain Boulton, Gregory, J.S.; Slaughter, C.; Moomaw, C.; Hsu, J.; Jence 249, 64-67, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 43-64;167-178, XX',180-183, XX',185 <BO2>
A;Residues: 43-64;167-178, XX',180-183, XX',185 <BO2>
A;Cross-references: UNIPARC:UP1000017558F; UNIPARC:UP10000175590
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA, cell Biol. 10, 505-514, 1991
A;Tille: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse
A;Reference number: A40466; MUID:91369479; PMID:1716439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: An insulin-stimulated protein kinase similar to yeast kinases involved in A;Reference number: A35061; MUID:90312137; PMID:2164259
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                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession. JC1451; A35061; A37140; A40466; S24947
C;Accession. JC1451; A35061; A37140; A40466; S24947
C;Accession. JC1451, A35061; A37140; A40466; S24947
C;Accession. JC1451; A35061; A37140; A40466; S24947
C;Accession: JC1451; MUID:93013050; PMID:1327976
A;Reference number: JC1451; MUID:93013050; PMID:1327976
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
                      Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - rat
N.Alternate_names: ERK1-MAP kinase; extracellular signal-regulated kinase
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C;Keyworde: DNA binding; homeobox; nucleus; transcription regulation
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Pred. No.
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Best Local Similarity 66.79
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A;Title: Molecular and developmental characterization of the heat shock cognate 4 gene c. A,Recerence number: A36333; MUID:90258915; PMID:2111451
A,Racesanion: A36333; MUID:90258915; PMID:2111451
A,Racesanion: A36333; MUID:90258915; PMID:2111451
A,Racesanion: A36333; MUID:90258915; PMID:2111451
A,Racesanion: DNA
A,Residuae: 1-651 < PRE>
A,Residuae: 1-651 < PRE>
A,Gene: Flyasse: HBC70-A
A,Gene: Flyasse: HBC70-A
A,Gene: Flyasse: Flyasse: FBgn0001219
C,Function: A,Gene: Flyasse: FBgn0001219
C,Function: Involved in protein folding and assembling/disassembling of protein complicion: C,Superfamily: bcr protein
C,Superfamily: bcr protein
C,Superfamily: bcr protein
C,Superfamily: MDE-ATP; molecular chaperone; nucleus
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NyAlternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
(Species: Bos prindgenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; $29270; A46098; PS0338
S;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinasi
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecula type: mRNA
A;Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PID
B;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
B;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
A;Stumpo, D.J.; Graff, J.M.; Albert, M.J.
A;Title: Molecular cloning, Characterization, and expression of a cDNA encoding the "80-A;Reference number: A32904; MUID:8926453; PMID:2726763
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A;Residues: nucleic and
A;Residues: 1-98, 'Q', 100-135 csr2>
A;Residues: 1-98, 'Q', 100-135 csr2>
A;Residues: 1-98, 'Q', 100-135 csr2>
A;Croser-references: UnitPARC:UPIO100017750A; GB:M24638; GB:M23738
B;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protein A;Reference number: S29267; MUID:93011168; PMID:1396720
A;Reference number: S29267; MUID:93011168; PMID:1396720
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A;Residues: 191-253, SEE', 257-279, 283-292, 'V', 294, 'PEQE', 299, 'A', 300, 'A', 302-313,'A', 315
A;Residues: 191-253, SEE', 257-279, 283-292, 'V', 294, 'PEQE', 299, 'A', 300, 'A', 302-313,'A', 315
A;Cross-references: UNIPARC:UP1000017750B
B;Menenti, S., Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
J. Biol. Chem. 268, 6878-6881, 1993
A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
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R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with A;Reference number: PS0338; MUID:92171958; PMID:1540183
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A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
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Pred. No. 1.2e+02;
1; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           632 AGAAGAAGAGGAGP 645
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Best Local Similarity 64.3
Matches 9; Conservative
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NyAlternate names: silk fibroin, dragline
C;Species: Nephila clavipes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A44112; S27824
E;Hinman, M.B.; Lewis, R.V.
J. Biol. Chem. 267, 19320-19324, 1992
A;Fitle: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
A;Fitle: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
A;Fitle: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
A;Fitle: Isolation of a clone encoding a second dragline silk fibroin: Nephila clavipes
A;Fesidues: 1-627 - AIN.
A;Fesidues: 1-627 - AIN.
A;Fesidues: 1-627 - AIN.
A;Coss-references: UNIPROT:P46804; UNIPARC:UPIO000135DC6; GB:M92913; NID:gl59713; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIP:113893)
B;Hinman, M.B.; Lewis R.V.
cubmitted to the EMBL Data Library, May 1992
A;Defenced and Cost and Cost
                                                                                                                                                                                                        Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

Nature 402, 761-768, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: A36333
R;Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.; Perrimon, N.; Craig, E.A. Mol. Cell. Biol. 10, 3232-3238, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                               hypothetical protein At2g27470 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnaK-type molecular chaperone Hsc70-4 - fruit fly (Drosophila melanogaster)
N;Alternate names: heat shock cognate protein 70
C;Species: Drosophila melanogaster
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 31-Dec-2004
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Pred. No. 1.2e+02;
1; Mismatches 4; Indels
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A)Accession: S27824
A)Molecule type: mRNA
A)Residues: 19-627
A)Cross-references: UNIPARC:UPI000017BE0B; EMBL:M92913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Pred. No.
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76.98;
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity
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A; Cross-references: UNIPARC: UPI000017750D; UNIPARC: UPI000017750E; UNIPARC: UPI000017750F; 514
A; Experimental source: brain
A; Mix perimental source: brain
A; Mote: this sequence is identical with that of myristoylated alanine-rich C-kinase subst; Comment: This protein is a major cellular substrate for protein kinase C and plays a r c; Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a c; Genetics:
A; Introns: 34/3
C; Superfamily: neurofilament triplet H protein
C; Superfamily: neurofilament blocked amino end; calmodulin binding; lipoprotein; myristyla F; 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F; 2/Modified site: myristylated selves (Ser) (covalent) (by protein kinase C) #status
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MUCLING-1914;
MEDLING-19203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
MEDLING-17., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S., Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
"A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY
06h6a6
086pil
096dh1
06dh1
06dh1
09h7p9
09m2x
065288
056288
0692k9
0692k9
0692k9
0692k9
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Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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              Q86PII_TOXGO
Q96D18_HUMAN
Q6DHV6_HUMAN
Q9H7P9_HUMAN
Q9M4X9_CHLRE
NLGN2_HUMAN
NLGN2_RAT
                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                          QSF288 MOUSE
Q69ZK9 MOUSE
Q94LU4 ORYSA
Q9DCH0 MOUSE
                                                                                                                                                                    CHICK
F9 BURPS
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                                                                                                                                                                                                                                                                                                                            Created)
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Name=CTAG1B; Synonyms=CTAG, CTAG1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2002 (TrEMBLrel, 22, Hypothetical protein LAGE-2
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Q9NY13;
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Best Local Similarity
 Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  Name=LAGE-2;
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RESULT 1
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                                                                                                          (without alignments)
97.196 Million cell updates/sec
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                                                                                          March 13, 2006, 18:53:23 ; Search time 108.882 Seconds
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Maximum Match 100%
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CTGG2 HUMAN STANDARD; PRT; 210 AA.

O75638; O75637; Q9BUBO; Q9UJ89; Q9Y479;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
Name-CTAG2; Synonyms-ESO2, LAGE1;
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T.;
de Plaen B., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
"LAGE-1, Cancer 76:903-908(1998).
                 "Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99325550, PubMed=10399963; Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.; Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.; Interleukfin-2-induced, melanoma-specific T cells recognize CAMEL, unexpected translation product of LAGE-1."; Int. J. Cancer 82:442-448(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-199454989; Dubmed-10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
DNA methylation is the primary silencing mechanism for a set
line- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 197327-7338(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.015;
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Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lethe B.G.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                     Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF277315; AAL27014.1; -; Genomic_DNA.
EMBL, AJ275977; CAB76943.1; -; Genomic_DNA.
EMBL, AF277315; AAL27013.1; -; Genomic_DNA.
SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B)
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MEDLINE=98289662; PubMed=9626360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Submitted (JUL-2001)
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                                                                                                                  NUCLEOTIDE SEQUENCE
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Nelson D.L.;
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                                                                                                                                                                                                                                               Platzer M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
                                                                                                               Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano de Plaen E., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908 [1998].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB 1; Length 180;
Pred. No. 0.015;
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-!- SIMILARITY: Belongs to the CTAG family.
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Gly-rich.
B122C5C2C8BE1569 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997)
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Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
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EMBL; AF038567; AAD05202.1; -; mRNA.
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                                                                                           MEDLINE=98289662; PubMed=9626360;
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Matches 15; Conservative
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LIAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
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MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                               some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and head and neck cancers.
                                                                                                                                                                                                                                                                                                               DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing; Antigen; Polymorphism; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR 007857.
8BE0EE00AE55E8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform LAGE-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R -> Q.
/FTId=VAR_007855.
E -> Q.
/FTId=VAR_007856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VSP_004301.
                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the CTAG family.
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ223093; CAA11117.1; -; Genomic DNA.
EMBL; AJ223093; CAA1116.1; -; Genomic_DNA.
EMBL; AJ223040; CAA11043.1; -; mRNA.
EMBL; AJ223041; CAA11044.1; -; mRNA.
EMBL; AJ012834; CAA10194.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC002833; AAH02833.1; -; mRNA.
Ensembl; ENSG00000126890; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gly-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W -> R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 AA; 21120 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ012835; CAA10196.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-InvDB; HIX0017163; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC; HGNC:2492; CTAG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
188
210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                   TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183°
135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC002833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 300396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPBIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPBIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

Ray Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

Ray Basley O.P., Bird C.P., Barkes K.N., Beard L.M., Beare D.M.,

Ray Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Terankland J.A., Fraser A., French L., Garner P.,

Ray Bilington A.G., Frankland J.A., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Andrewood S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

AND M.B., Kimberley A.M., King A., Kriights A., Laird G.K., Lawlor S.,

Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

A Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showheen R., Sims S.,

Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Wallis J.M.,

Mitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whittehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Williming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

Nore R. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871 (2001).
-!- SIMILARITY: Contains 2 ANK repeats.
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00248; ANK; 2.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS500299; UBIQUITIN 1; FALSE_NEG.
PROSITE; PS50053; UBIQUITIN 2; 1.
ANK repeat; Hypothetical protein; Polymorphism; Repeat.
                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                    337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL354776; CAC17565.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P42771; 2A5E.
Ensembl; ENSG00000124227; Homo sapiens.
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC; HGNC:16217; C20orf86.
InterPro; IRR0062110; ANK.
InterPro; IPR000626; Ubiquitin.
Pfam; PP00023; ANK; 2.
                                                                                                                                                                                                                                                            Hypothetical protein C20orf86.
                         PRINTS; PR01415; ANKYRIN.
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                   Name=C20orf86;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                  CT086_HUMAN
                                                                                                                                                                      Q9BZ19;
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Gaps

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1; Indels

89.7%; Score 70; DB 1; Length 210; 93.3%; Pred. No. 0.19;

Pred. No. 0.19; 0; Mismatches

Ouer, ...
Best Local Similarity
...rhes 14; Conservative

Query Match

Query Match

Matches

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RESULT 6 08780

VARIANT

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REPEAT DOMAIN REPEAT

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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAINERS 13.

TOTAL STATE AND STATE 
                                                                                                                                                                          Oryza sativa (Rice).
Sukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AD44404; AAK50601.1; -; Genomic_DNA.
Gramene; Q94LD1; -.
InterPro; IPR007228; DUF390.
InterPro; IPR007228; Transposase_28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
                                               Created)
Last sequence update)
Last annotation update)
  867 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.5%; Score 55; DB 66.7%; Pred. No. 63; ive 1; Mismatches
                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last annot
Hypothetical protein OSJNBa0026A15.11.
Name-OSJNBa0026A15.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 AGGSRAGGPGGGGSR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q63QT8_BURPS PRELIMINARY;
Q63QT8;
Q94LD1 ORYSA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B., Jin S.S., Koo H., Ziamann V., Haiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Wakaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AC023188; AAM22719.1; -; Genomic_DNA. EMBL, AAE017090; AAP53592.1; -; Genomic_DNA. Gramene; QBL680; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 559;
                                                                                                                                                                          Length 337;
                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 559 ÅA, 58950 MW, A5B4492C2D3F94FA CRC64;
                                                                                                                        EC8BA4AD414756CB CRC64;
                                                                         R -> C (in dbSNP:584855).
/FTId=VAR_014400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                          ; DB 1;
; 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.5%; Score 55; DB 2;
66.7%; Pred. No. 42;
ilve 1; Mismatches 4
Ubiquitin-like.
ANK 1.
ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          559 AA.
                                                                                                                                                                       70.5%; Score 55; DB 73.3%; Pred. No. 27; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seque
01-FEB-2005 (TrEMBLrel. 29, Last annot
Hypochetical protein OSJNBa0011L09.12.
ORFNames=OSJNBa0011L09.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007228; DUP390.
InterPro; IPR007321; Transposase_28.
Pfam; PF04094; DUF390; 2.
Pfam; PF04195; Transposase_28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                           337 AA; 36714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :| ||||| |
276 AGGSRTSGPGGGGSR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                             1 AGAARASGPGGGAPR 15
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                                                                                                                                                                                                                                                                                                          || |||:|| ||| |
AGGARAAGPTGGASR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBL680_ORYSA PRELIMINARY;
                                                                                                                                                                                               Local Similarity 73.3
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Matches 10; Conservative
  164
241
273
287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39947;
  88
211
244
287
                                                                                                                           SEQUENCE
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Buell

Query Match

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Q94LD1 ORYSA

RESULT 7

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Gaps

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DR RE BR BR SO ST SO ST

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                           STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Higgs D.R.;
"Sequence, structure and pathology of the fully annotated terminal
Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
Ensembl; ENSG0000167933; Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                              dehalogenans 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339; Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                       Anaeromyxobacter denalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                                                                          Larimer F., Land M.; "Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54, DB 2; Length 895;
Pred. No. 88;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.9%; Score 53; DB 2; Length 321; 66.7%; Pred. No. 47;
                                                                                                                                                                                                                                                                      Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAHD01000013; EAL79351.1; -; Genomic DNA.
SEQUENCE 895 AA; 93871 MW; 0AE25BBBF172BDB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gene X.
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                                                                                                                                                                                                                                                                                                                                    STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
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1 Similarity 73.3%;
11; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O96S27 HUMAN PRELIMINARY;
O96S27;
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                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                      NCBI_TaxID=290397;
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Best Local Similarity
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PubMed=1537793; DOI=10.1073/pnae.0403306101;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Reldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J., Mattrin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M.;

"Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. US.A. 101:14246-14251(2004).

EMBL. CP000010; AAU49707.1; -; Genomic_DNA.
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerses III, delta subunit (EC 2.7.7.7).
Name=holA; OrderedLocusNames=BMA2451;
Burkholderia mallai (Pseudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA. GO:0006260; P:DNA replication; IEA. InterPro; IPR010372; DNA pol3 delta. InterPro; IPR0599; DNA pol3 delta. InterPro; IPR0599; DNA polIII delta. Pf06144; DNA pol3 delta; I. TIGRFAMS; TIGR01128; holA; 1.
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GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
GO; GO:000560; F:transferase activity; IEA.
GO; GO:000560; P:DNA replication; IEA.
InterPro; IPR010372; DNA pol3 delta.
InterPro; IPR05790; DNA pol1I delta.
Pfam; PP06144; DNA pol3 delta; I.
TIGRFAMS; TIGR01128; holA; I.
Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                      Length 362;
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                                                                                                                                           362 AA; 38726 MW; DSFF3DE783D41E41 CRC64;
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Last annotation update)
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. 38;
                                                                                                                                                                                    Score 54; DB 2;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                  362 AA.
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Pred. No.
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83.3%;
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83.3%;
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(TrEMBLrel. 31, I
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04NUK4 9DELT
ID 04NUK4 9DELT PRELIMINARY;
AC 04NUK4;
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31,
DE LigA.
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Q62H22;
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348 ARAAGPGGDAPR 359
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Best Local Similarity 83.3'
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                                                                                                                          Complete proteome. SEQUENCE 362 AA;
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les 10; Conserv
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72444 MW; DDB97FC0C40C23F8 CRC64;

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644 AA;
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SEQUENCE
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Chow T.-Y., Hsing Y.-I.C., Chen H.-C., Chen S.-K., Chen T.-R.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Cheng C.-H., Chung C.-H., Hans S.-Y., Lee M.-C.,
Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
Li Y.-F., Lin Sr-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
"Oryza sativa BAC OSJNBb0012621 genomic sequence.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AC135421; AAU10755.1; -; Genomic_DNA.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                Ucda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Morimura K., Ikeda H., Hattori M., Beppu T.;
Morimura K., Ikeda H., Hattori M., Beppu T.;
Morimura K., Ikeda H., Hattori M., Beppu T.;
Mclanome sequence of Symbiobacterium thermophilum, an uncultivable
bacterium that depends on microbial commensalism.";
Nucleic Acids Res. 32-4937-4944(2004).

EMBL, AP006840; BAD40403.1; -; Genomic_DNA.
GO, GO:0004665; F: prephenate dehydrogenase (NADP+) activity; IEA.
GO, GO:0006571; P:tyrosine biosynthesis; IEA.
InterPro; IPR03099; Prephen_dehydrog.
Pfam; PF02153; PDH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AA; 32843 MW; 09A06ACOAFA734EC CRC64;
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Last annotation update)
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                                                                    322 AA
                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Symbiobacterium.
                                                                                                                                                                                                                                                                                                                                        STRAIN=IAM14863;
PubMed=15383646; DOI=10.1093/nar/gkh830;
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25-007-2004 (TrEMBLrel. 28, Last seques-
25-007-2004 (TrEMBLrel. 28, Last and
Hypothetical protein OSJNBb0012G21.2.
Name-OSJNBb0012G21.2;
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                                                                    PRT;
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                                                                                                          25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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Q688J5 ORYSA
ID Q688J5, ORYSA PRELIMINARY;
AC Q688J5; ORYSA PRELIMINARY;
                                                               QG7PJO_SYMTH PRELIMINARY;
Q67PJO;
                                                                                                                                                                                                      OrderedLocusNames=STH1418
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                                                                                                                                                                                 Prephenate dehydrogenase
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                     RESULT 12
C67PJ0_SYN
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelimae; Anopheles.
NCBI_TaxID=180454;
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The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:000815; C:integral complex; IEA.
GO; GO:000515; F:protein binding; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
GO; GO:0007259; P:integrin-mediated signaling pathway; IEA.
InterPro; IPRO0041; Integrin_alpha.
Pfam; PF01839; FG-GAP; 3.
PRINTS; PR01185; INTEGRINA.
SWART; SW00191; Int alpha; 1.
SWART; SW00191; Int alpha; 6.
Cell_adhesion; Integrin; Transmembrane.
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Length 644;
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SEQUENCE 1379 AA; 149836 MW; 2D6945E834F3DD75 CRC64;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Score 53; DB;
Pred. No. 88;
1; Mismatches
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ORFNames=AdehDRAFT 1169;
Anaeromyxobacter dehalogenans 2CP-C.
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13-SEP-2005 (TYEMBLYEL) 31,
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STRAIN=2CP-C;
STRAIN=2CP-C;
Copeland A., Lucae S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              7;
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBL_TaxID=290397;
                                                                                                                                                                                                                                                                        Query Match 67.3%; Score 52.5; DB 2; Length 924; Best Local Similarity 59.1%; Pred. No. 1.46+02; Matches 13; Conservative 1; Mismatches 1; Indels 7
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Search completed: March 13, 2006, 19:14:26 Job time: 111.882 secs

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Sequence 15, Appl
Sequence 30, Appli
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Sequence 5, Appli
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Sequence 17335, A
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Sequence 10, Appl
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Sequence 23998,
Sequence 31759,
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                                                                                                                             March 13, 2006, 19:14:49; Search time 27.8824 Seconds (without alignments) 44.477 Million cell updates/sec
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Sequence 25, 7
Sequence 15, 7
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Sequence 8,
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-392-714-25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
US-09-252-991A-20577

US-09-252-991A-31279

US-10-104-047-3295

US-09-252-991A-19800

US-09-252-991A-20512

US-09-417-197-57

US-09-417-197-57

US-09-252-991A-20165

US-09-252-991A-21865

US-09-252-991A-21865

US-09-252-991A-21865

US-09-252-991A-20125

US-09-464-377-3

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US-08-468-291A-4

US-08-589-619-4

US-08-209-147-37
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APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                    US-08-317-844B-26
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: L0461/7005
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-3441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Wolf, Greenfield & Sacks,
600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
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TOPOLOGY: 1:0.0.10

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Matches 15; Conservative
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CLASSIFICATION: 435
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COUNTRY:

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APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer TITLE OF INVENTION: Truncated Proteins, Uses Thereof, TITLE OF INVENTION: Binding Peptides Derived Therefrom NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAARASGPGGGAPR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-937-263B-8
US-08-937-263B-8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 78; DB 2; Length 180;
100.0%; Pred. No. 0.01;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew J.
APPLICANT: Gare, Ali O.
APPLICANT: Williamson, Barbara
APPLICANT: Williamson, Barbara
APPLICANT: Williamson, Barbara
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses:
TITLE OF INVENTION: Therefor
FILE REFERENCE: L0461/7062
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER APPLICATION NUMBER: PCT/US98/14679
SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
ZUCOMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
AMBIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION NUMBER: 09/05,422
FILING DATE: 06.0ctober 3, 1996
ATTORNEY AGENT INFORMATION:
NAME: HANSON, NO. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10,5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
SEQUENCE CHARACTERISTICS:
                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09392714A Patent No. 6686147
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
US-09-392-714-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-392-714-25
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    <151> 1998-01-27
                                                                                                                                                                                              th 100.0%; Score 78; DB 2; Length 180; I Similarity 100.0%; Pred. No. 0.01; 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.01;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
ITILE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES:
CORRESSEDNIENCE ADDRESS:
ADDRESSEBE: Wolf, Greenfield & Sacks, P.C.
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APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV);
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
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PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 30, Application US/09849602
; Patent No. 6794501
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Patent No. 5811519
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Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                     Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                         US-09-341-829A-9
                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-791-495-7
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                                                                                          LENGTH:
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                                                                                                   APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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ZIP: 1015

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMFUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,546D

FILING DATE: 02-0ct-1998

CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 6723832man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.01;
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APPLICANT: Lucas, Sophie
APPLICANT: Ducas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPREBRUCE: LO461/706
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATE:

APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: OCCODER 3, 1996
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
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                                     Sequence 15, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 180 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: USA
                    US-09-165-546D-15
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Wolf, Greenfield & Sacks, P.C.
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                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Van Ameterdam, John R.
REGISTRATION UNDRER: 40,212
REFERENCE/DOCKET NUMBER: 1.0461.
TELECOMMUNICATION INFORMATION:
TELEFANE: 617-720-3500
TELEFAN: 617-720-3500
TELEFAN: 617-720-2441
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
                    600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.78;
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Best Local Similarity 93.33,
Best Local 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                    STREET: 600 PCITY: Boston
                                                                             COUNTRY: USA
ZIP: 02210
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-341-829A-5
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LENGTH: 210
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Patent No. 6794131

GENERAL INFORMATION:

APPLICANT: Leth., Bernard

APPLICANT: Leth., Charles

APPLICANT: Godelaine, Daniele

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS

FILE REPRENCE: L0461/7066

CURRENT APPLICATION NUMBER: US/09/341,829A

CURRENT PILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: PCT/US98/01445

PRIOR APPLICATION NUMBER: PCT/US98/01445

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FRSESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.3%; Pred. No. 0.098;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

89.7%; Score 70; DB 2; Length 180;
Best Local Similarity 93.3%; Pred. No. 0.098;
Matches 14; Conservative 0; Mismatches 1; Indels
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; Patent No. 5811519
; GENERAL INFORMATION:
    APPLICANT: Leth, Bernard
    APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Li-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
                                                                                                                     L0461/7005
APPLICATION NUMBER: US/08/791,495
APFLICATION: 435
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VOR AMKLECTAM, JOHN R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-720-2840
TELEPAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAARASGPGGGAPR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 AGAARASGPRGGAPR 62
                                                                                                                                                                                                                                        LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-341-829A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                        US-08-791-495-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/09341829A
; Batent No. 6794131
; GENERAL INFORMATION:
   APPLICANT: Lucth,, Bernard
; APPLICANT: Lucth, Sophie
   APPLICANT: Lucas, Sophie
   APPLICANT: De Smet, Charles
   APPLICANT: De Smet, Thierry
   TILE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
   FILE REFERENCE: L0461/7066
   CURRENT APPLICATION NUMBER: US/09/341,829A
   CURRENT FILING DATE: 1999-10-18
   PRIOR APPLICATION NUMBER: US/09/341,495
   PRIOR APPLICATION NUMBER: PCT/US/98/01445
   NUMBER OF SEQ ID NOS: 14
   NUMBER OF SEQ ID NOS: 14
   NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70; DB 1; Length 210; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.7%; Score 70; DB 2; Length 210; Best Local Similarity 93.3%; Pred. No. 0.11; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Partentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
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Gaps

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RESULT 15
US-09-902-540-13196
; Sequence 13196, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                           Score 50; DB 2; Length 160;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.1%; Score 50; DB 2; Length 366; 66.7%; Pred. No. 54; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                               1; Mismatches
     PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17249
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: March 13, 2006, 19:18:50 Job time : 27.8824 secs
                                                                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249
                                                                                                                                                                                                                                                                           64.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13196
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72 AGTAPAAGPGATAPR 86
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SEQ ID NO 13196
LENGTH: 366
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 66.79
Matches 10; Conservative
                                                                                                                                                                     TYPE: PRT
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                                              PAGENTA NO. 6551757

BARGEL NO. 6551757

GENERAL INFORMATION: Under al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24923, Application US/09252991A
Patent No. 6551795
GENERAL INCORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24923
LENGTH: 210
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APPLICANT: Warc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION, NUMBER: US 60/074,788
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                           Sequence 17335, Application US/09252991A
Patent No. 6551795
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-24923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 AGAGRAAGPGTGQPR 291
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US-09-252-991A-17335
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Gaps

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75, Appl 834, App 75, Appl 7, Appli 75, Appli 75, Appl 75, Appl 76, Appl 76, Appl 76, Appl

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 76, Appl Sequence 496, App

Sequence Sequence Sequence

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

Result

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APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, lan A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REPRENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILIG DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR RPLICATION NUMBER: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin Version 3.2
SEQ ID NO 1404
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 78; DB 4; Length 30; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 15; Conservative 0; Mismatches 0; Indels
US-10-296-734-1436
US-10-1296-734-1438
US-10-188-822-141
US-10-1188-822-141
US-10-1146-473-69
US-10-117-937-75
US-10-117-937-75
US-10-67-022-75
US-11-067-059-75
US-10-117-937-76
US-10-657-022-76
US-10-657-022-76
US-10-657-031-88
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Sequence 202, Application US/10482029
Sequence 202, Application US/10482029
Sequence 202, Application US/10482029
Sequence 202, Application US/10482029
STATLE OF INVENTION: Oncology drug innovation
TITLE OF INVENTION: Oncology drug innovation
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 202
LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-313-986-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1404, Application US/10296734; Publication No. US20040054137A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: NYSOla segment
US-10-296-734-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAARASGPGGGAPR 15
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       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-10-296-734-1404
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       RESULT 2
       80012645978666644444
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Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1404, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                              March 13, 2006, 19:51:56; Search time 90.7059 Seconds (without alignments) 69.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Sequence 3, As Sequence 386, Sequence 382, Sequence 139, Sequence 11, Sequence 15, Sequence 11, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description,
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Sequence 27
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Sequence 8
Sequence 7
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Sequence 7
Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA Main:*

cgn2_6/ptodata/1/pubpāa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-482-029-202
US-09-849-602-88
US-09-849-602-88
US-10-027-655-71
US-10-207-655-71
US-10-107-937-74
US-10-107-937-74
US-10-107-937-74
US-10-107-937-74
US-10-108-139
US-10-296-734-832
US-10-188-139
US-10-751-088-15
US-10-751-088-15
US-10-751-088-15
US-10-837-217-11
US-10-837-217-11
US-10-877-217-127
US-10-877-217-138-11
US-10-877-217-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1867569 segs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       1 AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                        US-09-529-206E-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STRIE: New York
COUNTRY: USA
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        ; Score 78; DB 5; Length 179; Pred. No. 0.068; 0; Mismatches 0; Indels
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Pred. No. 0.068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: 0ccober 3, 1996
FILING DA
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SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09751798
Patent No. US20020010321A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
                                                                                                                                                                            1 AGAARASGPGGGAPR 15
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Query Match
Best Local Similarity 100.0
Matches 15, Conservative
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TOPOLOGY: linear
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RESULT 4
US-09-409-602-30
Sequence 30, Application US/09849602
Publication No. US20030165834A1
GENERAL INFORMATION
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.

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Gaps
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Sequence 8, Application US/10023182
Publication No. US20020164665A1
GENERAL INPORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
APPLICANT: Stockert, Elisabeth
TITLE OF INVENTION: Colon Cancer Antigen Panel
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (DRV)
CURRENT APPLICATION NUMBER: US/09/849, 602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NOS: 30
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OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                        APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFERENCE: CTLIMM.21CPIC
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT PILING DATE: 2001-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR PRIOR NUMBER: PCT/USO1/13806
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR FILING DATE: 2000-04-28
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100.0%; Pred. No. 0.068;
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Publication No. US20030220239A1

GENERAL INPORMATION:

APPLICANT: CTL IMMUNO THERAPIES CORP.

APPLICANT: SIMARD, John, J.L.

APPLICANT: LIDANOND, David, C.

APPLICANT: LIU, Liping

TITLE OF INVENTION: EPITOPE SEQUENCES

FITLE REFERENCE: CTLIMM. 027A

CURRENT APPLICATION NUMBER: US/10/117,937

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/282,211

PRIOR APPLICATION NUMBER: US 60/337,017

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 180
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Sequence 14, Application US/10364614

Publication NO. US20030175250A1

GENERAL INFORMATION:
APPLICANT: JAGER, Elke
APPLICANT: Glatic, Sacha
TILLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
FILE REFERENCE: LUD 5726.1 Clp
CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT PILING DATE: 2002-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR APPLICATION NUMBER: US 60/355,828

NUMBER OF SEQ ID NOS: 17

SOFTWARE PLING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                  Sequence 71, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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100.0%; Score 78; DB 4; Length 180;
100.0%; Pred. No. 0.068;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
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Best Local Similarity 100.0
Matches 15, Conservative
                                                      15; Conservative
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US-10-207-655-71
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ORGANISM: Homo sapiens
                        Best Local Similarity
Matches 15; Conserv
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LENGTH: 180
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LENGTH: 180
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  Query Match
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LENGTH: 180
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APPLICANT: Hever, A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Watenon, Susan R.
APPLICANT: Watenon, Susan R.
APPLICANT: Watenon, Susan R.
APPLICANT: Watenon, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-01250007
CURRENT APPLICATION NUMBER: US 109/663,733
PRIOR PILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
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PRIOR PLING DATE: 2001-12-29
PRIOR PLING DATE: 2001-12-14
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PRIOR PLING DATE: 2001-12-14
PRIOR PLING DATE: 2001-12-14
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-02-03
PRIOR PLING DATE: 2002-02-04
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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100.0%; Pred. No. 0.068;
ive 0; Mismatches 0; Indels
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Publication No. US20040054137A1

GENERAL INFORMATION.

APPLICANT: Thompson, Scott A

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR PLING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: PATENTING DATE: 2000-05-26

SOFTWARE: PATENTING DATE: 2000-05-36

SOFTWARE: PATENTING DATE: 2000-05-36
                     Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                            APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAARASGPGGGAPR 15
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ORGANISM: Homo sapiens
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US-10-296-734-832
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GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Bos Biotechnology, Inc.

ITILE OF INVENTION: Methods of Diagnosis of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: Cancer

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: Cancer

FILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US 60/302, 814

PRIOR PELING DATE: 2001-01-03

PRIOR PELING DATE: 2001-01-08

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/372, 246

PRIOR PELING DATE: 2002-04-12

PRIOR PELING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 207

SOFTWARE: Patent IN Ver. 2.1

FEMALE PATENTING DATE: 2002-04-12

SOFTWARE: Patent IN Ver. 2.1
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Publication No. US20040132088A1
Publication No. US2004013208BA1
Publicant Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK.0221
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT FILING DATE: 2004-02-10
PRIOR FILING DATE: 2002-11-07
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Pred. No. 0.068;
Mismatches 0; Indels
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                                                                                    ; OTHER INFORMATION: NYNSOla consensus polypeptide US-10-296-734-832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 119, Application US/10188832; Publication No. US20040076955A1; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 15; Conservative 0;
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Artificial
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US-10-777-053-11
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                                                                                                                                                                                                                                                  APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNK.032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR PILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 180
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; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Knuth, Alexader; Jager, Elker, Gerd
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/165,546D FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTHARE: WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILLING DATE: 02-Jan-2004
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 66 Fifth Avenue
CITY: New York City
STATE: New York
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SEQ ID NO 11
LENGTH: 180
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SEQUENCE DESCRIPTION: SEQ ID NO: 15
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NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-751-088-15
Sequence 15, Application US/10751088
Sublication No. US20040188044A1
GENERAL INFORMATION:
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TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 180 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                      TYPE: PRT
CORGANISM: Homo Sapien
US-10-777-053-11
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TYPE: PRT
ORGANISM: Homo sapiens
RESULT 2
US-11-021-441-28
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 SEQ ID NO 7
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Sequence 20556, A
Sequence 20334, A
Sequence 22333, A
Sequence 22332, A
Sequence 22661, A
Sequence 2786, A
Sequence 2788, A
Sequence 17631, A
Sequence 25787, A
Sequence 25787, A
Sequence 17631, A
Sequence 25787, A
Sequence 25786, A
Sequence 25787, A
Sequence 34, Appl
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                                                                                                    March 13, 2006, 19:54:06; Search time 10.2353 Seconds (without alignments) 40.793 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USI0_NEW_PUB.pep:*
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                 161667 seqs, 27834885 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                1 AGAARASGPGGGAPR 15
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Maximum DB seq length: 2000000000
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No.
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38, Appl
38, Appl
65, Appl
1240, Ap
108, App
107, App
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26217, A
14205, A
24201, A
8816, Ap
14203, A
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19985, A
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Sequence 1
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Sequence
US-11-087-099-6009
US-11-096-568A-27265
US-11-0931-198-38
US-10-921-793-38
US-10-921-793-38
US-11-198-38
US-11-186-284-65
US-11-129-143-108
US-11-129-143-108
US-11-129-143-108
US-11-129-143-108
US-11-129-143-108
US-11-096-568A-24201
US-11-096-568A-14203
US-11-096-568A-14203
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US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19986
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Sequence 28, Application US/11021441
| Publication No. US20050249748A1
| Publication No. US20050249748A1
| GENERAL INFORMATION
| APPLICANT: DUBENSKY, Thomas W., Jr.
| APPLICANT: DUBENSKY, Thomas W., Jr.
| APPLICANT: COCK, David N.
| APPLICANT: COCK, David N.
| TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF LINGATION NUMBER: US/11/021,441
| CURRENT APPLICATION NUMBER: US/11/22,34
| CURRENT PELLOATION NUMBER: US/616,750
| PRIOR FILING DATE: 2004-10-06
Sequence 7, Application US/11155288
Publication No. US20060008468A1
GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REFERENCE: MANNK. 050A
CURRENT APPLICATION NUMBER: US/11/155, 288
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR PELING DATE: 2004-06-17
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGAARASGPGGGAPR 15
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US-11-096-568A-22334
Sequence 22334, Application US/11096568A
Sequence 22334, Application No. US2060048240A1
Sequence 22334, Application No. US20600048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-096-568A-22333, Application US/11096568A

Sequence 2233, Application US/11096568A

Publication No. US20600648240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22333

LENGTH: 358
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                                                                                                                                                                                                                            Score 53; DB 7;
Pred. No. 3.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 7;
Pred. No. 3.8;
0; Mismatches
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i LOCATION: (1)..(358)
cother information: Ceres Seq. ID no. 12408543
US-11-096-5688-22333
                                                                                                     NAME/KEY: misc_feature
| LOCATION: (1)..(306)
| OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
i LOCATION: (1)...(353)
cother information: Ceres Seq. ID no. 12408544
US-11-096-5688-22334
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                                                   ORGANISM: Zea mays subsp. mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.9%;
Best Local Similarity 71.4%;
Matches 10; Conservative (
                                                                                                                                                                                                                               67.9%;
76.9%;
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89 GVARADGPGTGAP 101
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                                                                                                                                                                                                                                                                                                                                  2 GAARASGPGGGAP 14
                                                                                                                                                                                                                               Query Match 67.9
Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity
       LENGTH: 306
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GENERAL INFORMATION:

TITLE OF INVENTION: Theory

TITLE OF INVENTION: Theory

FILE REFERENCE: 2750-152280S2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

SEQ ID NO 20556
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Sequence 496, Application US/10623155

Publication No. US20850261166A1

GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.12.4 55.020
CURRENT APPLICATION NUMBER: US/10/623,155

CURRENT PILING DATE: 2003-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 78; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 15; Conservative 0; Mismatches 0; Indels
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84.6%; Score 66; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 13; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE; 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR APPLICATION NUMBER: US 10/883,599
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 496
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AGAARASGPGGGAPR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGAARASGPGGGAPR 15
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 275-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22661
LENGTH: 391
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592P032
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 167
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Pred. No. 9.9;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 48; DB 7;
68.8%; Pred. No. 18;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                               ) LOCATION: (1). 7(391)
; OTHER INFORMATION: Ceres Seq. ID no. 12409618
US-11-096-568A-22661
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i LOCATION: (1).:(167)
cother information: Ceres Seq. ID no. 13596390
US-11-096-5688-10542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-096-568A-10542
; Sequence 10542, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
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Best Local Similarity 73.3%;
Matches 11; Conservative (
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66 AGAARRAGPSAPGGAP 81
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.5
Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays subsp.
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                                                                                                                                                                           Sequence 22332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUGS
CURRENT APPLICATION: WOMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REPRENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22662
LENGTH: 359
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      Gaps
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.9%; Score 53; DB 7; 71.4%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (1)...(420)
; O'THER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)._(359)
OTHER INFORMATION: Ceres Seq. ID no. 12409619
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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; Sequence 22661, Application US/11096568A
; Publication No. US20060048240A1
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ORGANISM: Zea mays subsp. mays
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34 AGAARRAGPSAPGGAP 49
                                                                            112 GAARGOGPGGEOPR 125
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174 GAARGQGPGGEQPR 187
                                         2 GAARASGPGGGAPR 15
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  Conservative
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Best Local Similarity
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US-11-096-568A-22662
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Matches
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1 AGAARASGPGGGA 13
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US-11-096-568A-23806
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APPLICANT: Myeun
APPLICANT: Myeun
APPLICANT: Bard, Jonathan A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Raikweki, Elleen M.
APPLICANT: Raikweki, Elleen M.
APPLICANT: Jacobeen, Jack S.
APPLICANT: Sophia, Heidi
APPLICANT: Sophia, Heidi
APPLICANT: Sophia, Heidi
APPLICANT: Howland, David
TITLE OF INVENTION: Beta-Amyloid Peptide-Binding Proteins and Polynucleotides
TITLE OF INVENTION: Beta-Amyloid APPRICATO
TITLE REFERENCE: 31896-67300 (AHP98126P2 C1)
CURRENT APPLICATION NUMBER: US 004-07-16
FRIOR APPLICATION NUMBER: US 09/774,936
PRIOR PRILING DATE: 1998-10-14
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: US 09/060,609
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: US 09/060,609
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 09/060,609
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 09/060,609
PRIOR PRIOR FILING DATE: 1997-04-16
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                                                                                                                                                                 APPLICANT: MASCHO, YAGUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 064335-0191
CURRENT PEPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 2001-379298
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALENTIN VEr. 2.1
SEQ ID NO 3295
LENGTH: 678
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Publication No. US20050282999A9
GENERAL INFORMATION:
                                                                                          YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 214
                       IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3295
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APPLICANT:
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APPLICANT:
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Sequence 23806, Application US/11096568A
| Publication No. US20060048240A1
| Sequence 23806, Application No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Therby
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT PILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 23806
| LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-096-568A-2578B

Sequence 2578B, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592BUS

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 2578B
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Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1).7(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
) LOCATION: (1).7(287)
; OTHER INFORMATION: Ceres Seq. ID no. 13493532
US-11-096-568A-25788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 7
Pred. No. 25;
0; Mismatches
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Sequence 17631, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Zea mays subsp. mays
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ORGANISM: Zea mays subsp. mays
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75.0%;
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69 ARGAGPGAGAP 79
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us-09-529-206e-26.rapbn

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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1552PUS
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 17631
LENGTH: 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAATURE:

JOCATION: (1).__(293)

OTHER INFORMATION: Ceres Seq. ID no. 12359516

FEATURE:

NAME/KEY: misc_feature

JOCATION: (6).__(6)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (79).__(79)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (78).__(78)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (78).__(78)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (79).__(79)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (81).__(81)

OTHER INFORMATION: Xaa is any aa, unknown or other

JOCATION: (81).__(81)

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JOCATION: (81).__(81)

JOCATION: (81).__(81)
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ORGANISM: Zea mays subsp. mays
FEATURE:
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Search completed: March 13, 2006, 20:03:30 Job time: 10.2353 secs

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58.355 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                  2443163 seqs, 439378781 residues
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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geneseqp2003bs:* geneseqp2004s:* geneseqp2003as:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Add35564 Human NY-	Add35568 Human NY-	Add25510 Binding d	Adn39068 Cancer/an	Adj54139 Human NY-	Adm72815 Human NY-	Adm73418 CAG-3 pro	Adm73417 Human NY-		Adq10446 Autoimmun	Ads80926 Tumour as			Adz28913 NY-ESO-1	Adz42374 Immunogen	Aea35651 Human NY-	Adw99402 NY-ESO-1/	Aeb80047 Human NY-	Aae13122 NY-ESO-IC	Aau85130 Human mel
ADD35564	ADD35568	ADD25510	ADN39068	ADJ54139	ADM72815	ADM73418	ADM73417	ADQ18451	ADQ10446	ADS80926	ADW44353	ADY85096	ADZ28913	ADZ42374	AEA35651	ADW99402	AEB80047	AAE13122	AAU85130
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74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* 1: genesem109/

Database :

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; metanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide. AAY05986 standard; peptide; 14 AA (first entry) 16-AUG-1999 AAY05986; vaccine. **AA**Y05986

Homo sapiens. WO9918206-A2 15-APR-1999.

(USSH) US DEPT HEALTH & HUMAN SERVICES. Cancer antigen NY ESO1/CAG-3. 97US-0061428P. Wang RF, Rosenberg SA; WPI; 1999-277270/23. 08-OCT-1997;

98WO-US019609

21-SEP-1998;

Claim 25; Page 50; 88pp; English.

The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human BSO-1/CAG-3 (or CAG-3) ORF1 (see AAV05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAV05966), portions of them and their variants (see AAV05967-8F), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of

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the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays, and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HiA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                             Score 74; DB 2; Length 14;
Pred. No. 0.0051;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                     1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-277270/23.
                                                                                                                                                                                      return to a patient
                                                                                                                                                                                                                            Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine
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The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), and and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 97), are useful as cancer vaccines that protect against cancer. The invention provides; vectors and host cells (also useful as vaccines); a contisense oligonucleotides that inhibit expression of the cancer peptide. The cancer by administering a cancer peptide, with a mileoule. The cancer peptides that inhibiting cancer by administering a cancer peptide, with or without an inhibiting cancer petides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
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                  lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, ecritcal cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
derived from, cancers such as primary or metastatic melanoma, thymoma
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidhey cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                                                                                                                                             100.0%; Score 74; DB 2; Length 15; 100.0%; Pred. No. 0.0055; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                   AAY05979 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer antigen NY ESO1/CAG-3.
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                                                                                                                                                                                                                                                            1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                 GAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-1999 (first entry)
                                                                                                                                                                                                                    14; Conservative
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                                                                                                  return to a patient
                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                       Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05979;
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                                                                                                                                                                                                                    Matches
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several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to imped, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptide and polymucleotides are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, conceptagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HV (human cumunosficiency virus), hepatitis, influenza, Japanese encephalitis virus, betetin-Barr virus and respiratory synctytal virus), bacterial (e.g., infections caused by Neasseria, Meningococcal, Haemophilus, Streptococcal, Legionella and Mycobacterium or parasitic
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prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
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                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Savine, vaccine; cancer; viral infection; HIV; hepatitis C virus, viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection;
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                                                                                                                         100.0%; Score 74; DB 2; Length 20; 100.0%; Pred. No. 0.0071; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           AAU85105 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 27; 364pp; English.
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                                                                                                                                                                                                              1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                        7 GAARASGPGGGAPR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2002 (first entry)
                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NYNSOla segment 4.
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                                                                                                                            Query Match
Best Local Similarity
Matches 14; Conser
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                                                                                      Sequence 20 AA;
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                                              patient
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This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate with a composition including the proteasome; under conditions that support processing of the substrate by proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, proteasome; proteosoacide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation, where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine development or in the generation or expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunotherapy. The invention is also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epitope liberation, substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekkeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
(e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence a peptide derived from a parent protein used to construct a savine of
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                                                                                                                               5; Length 30;
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                                                                                                                           100.0%; Score 74; DB 5; 100.0%; Pred. No. 0.01; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                               ADK68648 standard; protein; 179 AA.
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                                                                                                                                                                                                    1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                            Similarity 100.
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N-PSDB; ADK68674.
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DIAMOND D C
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                                                                                          Sequence 30 AA;
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(LEIX/) LEI X.
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                                                       invention
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                                                                                                                           Query Match
Best Local 8
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(DIAM/)
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                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                               RESULT 5
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for activating T-cells against neoplastic cells, and cells infected with virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing target cells in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated cancer associated antigen - is used to develop products for diagnosis and treatment of cancers and for monitoring cancer therapy
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   antigen; NY-ESO-1; regression; progression; onset;
                                                                                                                                                                                 ;
                                                                                                                                                     100.0%; Score 74; DB 8; Length 179; 100.0%; Pred. No. 0.052; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knuth A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "potential myristorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      old LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                      AAW62584 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                       Cancer associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 3; 49pp; English.
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                                                                                                                                                                  ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; treatment; diagnosis
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                                                                                                                                                                                                                                     GAARASGPGGGAPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-286417/25.
                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                Local Similarity
es 14; Conserv
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                                                                                                                           Sequence 179 AA;
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Misc-difference
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                                                                                                                                                      Query Match
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                                                                                                                                                                   Best Loc
Matches
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describes LAGE-1 tumour associated protein (TAP). The present invention which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes LAGE-1 tumour associated protein (TAP). The present invention characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells care specific for complexes of an HLA molecule and a LAGE-1 TAP or an characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an especific for a LAGE-1 TAP comprising contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the
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of onset of a cancerous condition, comprising monitoring a sample from a parameter selected from NY-BSO partient with the cancerous condition for a parameter selected from NY-BSO 1 protein, a peptide derived from NY-BSO-1 protein and cytolytic T cells specific for the peptide and an NHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-BSO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents human NY-ESO-1, formerly known as LL-1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders,
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
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                                                                                                                                                                                                                                   100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 57-58; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW69665 standard; protein; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                      1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                             49 GAARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                 Conservative
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N-PSDB; AAV50348.
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                                                                                                                                                      therapeutic regime
                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                              Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             products for particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
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Query Match
Best Local Similarity
Matches 14; Conserv
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Unidentified
                                                                                                                                                                                                                                                         21-OCT-2004
                                                                                                                                                                                                                                                                         15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
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                                                                                                                                                                                                           The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and content antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides comprising ORF1, ORF2 (see CAY05966), portions of these peptides and their variants (see AAY05965).

AAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides concer the receiptent from development of cancer. The invention provides: vectors and host cells car transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods of the cancer peptide, useful in diagnostic and detection assays; and methods of the verthout an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, concerved from, cancers such as primary or metastatic melanoma, thymoma, carvical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, lymphoma, astroma, lung cancer, liver cancer, leukaemia, uterine cancer, lymphoma, astroma, lung cancer, liver cancer, leukaemia, uterine cancer, lymphoma, astroma, pancreatic, and thyroid cancers. Melanoma is cancer and adenocarcinomas such cancer and adenocarcinoma is cancer and adenocarcinomas such cancer and adenocarcinomas such cancer and adenocarcinomas such cancer and adenocarcinomas such cancer and aden
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                                                                                                                                                                                                                                                                                                                                                                              NY ESO-1/CAG-3 gene, CAG-3 gene, cancer antigen, human, leukaemia, non-Hodgkins lymphoma, Hodgkins lymphoma, lung cancer, metastasis, melanoma, adenocarcinoma, thymoma, colon cancer, uterine cancer, breast cancer, prostate cancer, covarian cancer; cervical cancer, bladder cancer, kidney cancer, pancreatic cancer, liver cancer; tumour, diagnosis, immunotherapy, therapy, vaccine, ORFI.
                                                                                                             Gaps
diagnosis and treatment of LAGE-1 associated disorders, particularly
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                                                                             100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
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                                                                                                                                                                                                                                                    AAY05965 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer antigen NY ESO1/CAG-3.
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                                                                                                          14; Conservative
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                                                                                          Similarity
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                                               Sequence 180 AA;
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                                                                                                                                                                                                                                                                                     AAY05965;
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang RF,
                                                                                             Local
                  tumours
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                                                                                                         Matches
                                                                                                                                                                                                                     RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytotoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Peptide presented by MHC Class I HLA-B7 and
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e= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Peptide presented by MHC Class I HLA-B44"
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/note= "Peptide presented by MHC Class I HLA-B52"
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                   Length 180;
100.0%; Score 74; DB 2; Length 180 100.0%; Pred. No. 0.052; Mismatches 0; Indels
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.e= "Peptide presented by
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e= "Peptide presented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Peptide presented by and HLA-B35"
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                                                                                                                                                                                                                                             AAY52430 standard; protein; 180 AA.
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... "Peptide F
                                                                                                                                                                                                                                                                                                                                                                                          Human tumour antigen NY-ESO-1.
                                                                                                    14
                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                         14; Conservative
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Gaps

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Length 180;

100.0%; Score 74; DB 3; Length 18 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels

GAARASGPGGGAPR 14 49 GAARASGPGGGAPR 62

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Sequence 180 AA;
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                               Peptide
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Query Match Best Local Similarity 100. Matches 14; Conservative RESULT 10 ઠે g note= "Peptide presented by MHC Class I HLA-A24 and HLA-'note= "Peptide (AAY52434) presented by MHC Class I HLA-Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes. old LJ; HLA-A24" "Peptide presented by MHC Class I HLA-B35" note= "Peptide presented by MHC Class I HLA-B52" "Peptide presented by MHC Class I HLA-B52' "Peptide presented by MHC Class I HLA-B52' 162. .170 /note= "Peptide presented by MHC Class I HLA-B52" "Peptide presented by MHC Class I HLA-B52 /note= "Peptide presented by MHC Class I HLA-B8" 139. .147 /note= "Peptide presented by MHC Class I HLA-A3" 159. .167 'note= "Peptide presented by MHC Class I HLA-B7" 'note= "Peptide presented by MHC Class I HLA-A3" "Peptide presented by MHC Class I Scanlan M, Alexander K, Chen Y, Claim 30; Fig 3; 49pp; English. (LUDW-) LUDWIG INST CANCER RES 98US-00062422. 98US-00165546. 99WO-US006875. .162 .133 .147 .163 .162 .170 .147 .167 145. .153 /note= 124. .1 /note= 138. .1 /note= | 154. .1(/note= 154. .1 /note= E, Jager E, Ritter G; 153. WPI; 2000-038483/03. N-PSDB; AAZ38380. WO9953938-A1 24-MAR-1999; 17-APR-1998; 02-OCT-1998; 28-OCT-1999 Peptide

concoding which was isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma especiamens and cell lines, and breast and blader cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY ESO-1 are bound by both MHC (major histocompatibility complex) class I molecules for presentation to T-cells. Peptides AAY52431-Y52434 bind to Class I HLA-2 molecules, thereby stimulating proliferation of cycotoxic T-cells, while peptides AAY5245-Y52440 bind collss I HLA-DRS3 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, bersat cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, prolls This sequence represents a human tumour antigen, NY-ESO-1, the cDNA

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GAARASGPGGGAPR 62
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                                                     Revised record issued on 21-OCT-2004 : Correction to feature table key
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RESULT 11

ö The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein tumour deading frame (ORF)-1 that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma) protein, a tumour-asociated antigen. The tumour-associated antigen and displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response. Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA. Gaps ò 100.0%; Score 74; DB 3; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels Klade C; Human tumour antigen, NY-ESO-1 protein. Schrier PI, Aarnoudse CA, Heider K, (BOEH) BOEHRINGER INGELHEIM INT GMBH Example 3; Page 62-63; 73pp; English. AAY70862 standard; protein; 180 AA. 99WO-EP007832 98EP-00119583 (UYHO-) UNIV HOSPITAL LEIDEN 1 GAARASGPGGGAPR 14 31-JUL-2000 (first entry) Local Similarity 100. nes 14; Conservative WPI; 2000-339685/29. N-PSDB; AAD00152. Sequence 180 AA; fusion proteins WO200023584-A1. Homo sapiens. 16-OCT-1998; 15-OCT-1999; 27-APR-2000. AAY70862; Query Match

Gaps

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Length 180;

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New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions.
                                                                                            Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
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                                                                                                                                                                                                                           note= "Potential O-phosphorylation site"
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                                                                                                                                                                               'note= "Potential N-myristoylation site"
                                                                                                                                                                                                     note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                     152. .172
/note= "Potential transmembrane domain"
                                                                        Human oesophageal cancer-associated antigen NY-ESO-1,
                                                                                                                                                                                                                                                                     note= "Potential O-phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                 (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOITNT TMC
                                                                                                                                                           Location/Qualifiers
          AAB03154 standard; protein; 180 AA
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                                                   23-OCT-2000 (first entry)
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                               AAB03154;
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                                                                                                                                        Homo
AAB03154
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Human, NY-ESO-1; HLA, human leukocyte antigen, CTL; cytotoxic T cell; HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.

AAB69946 standard; protein; 180 AA.

AAB69946

(first entry)

27-APR-2001 AAB69946;

Human NY-ESO-1 protein.

GAARASGPGGGAPR 62 1 GAARASGPGGGAPR 14

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14; Conservative

Matches

Query Match Best Local Similarity

Scanlan M;

Chen Y,

Knuth A,

Old LJ,

Jager E, Stockert E,

(LUDW-) LUDWIG INST CANCER RES. (SLOK) SLOAN KETTERING INST CANCER RES. (CORR) CORNELL RES FOUND INC.

99US-00359503.

23-JUL-1999;

14-JUL-2000; 2000WO-US019220.

WO200107917-A1 Homo sapiens.

01-FEB-2001.

This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a cDNA encoding this sequence was isolated from a cDNA can a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophagus Expression analysis demonstrated that NY-ESO-1 was expressed in oesophagus listue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myriscoylation sites and O-phosphorylation sites and that it antigen is useful as an immunogen when combined with an adjuvant, in both proteurs and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to oesophageal cancer cells. It can also be used to generate diagnostic or therapeutic agents

Sequence 180 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                  Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; human leukocyte antigen-determining region; disease progression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents cancer testis tumour antigen NY-ESO-1 dalso called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukcoyte antigen (HLA) binding peptide, which binds to class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
                                                                                                         Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
                                                                                                                                                                                                                                                                                                                         Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                      Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
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Pred. No. 0.052;
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                           AAG67164 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                   for diagnosing testicular tumors.
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                                                                                                                               cancer; testis tumour.
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                                                                                                                                                   Homo sapiens.
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                                                                   13-NOV-2001
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The sequence represents a human NY-ESO-1 tumour rejection antigen or precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukoryte antigen-determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC class II HLA-DR.NY-ESO-1/SSX-2 complex expressed on the surface of a cell cor present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the concer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the CD loodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper I cells.
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100.0%; Pred. No. 0.052;
iive 0; Mismatches (
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Location/Qualifiers
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N-PSDB; AAS02254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer anispan, NY SEO-I. The MHC-II epitopes (TC from NY SEO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP crestricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.
                                                                                                 Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Location/Qualifiers
Misc-difference 45. .47
/note= "Encoded by CCCGGGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001WO-US002765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-496851/54.
N-PSDB; AAD14179, AAD14180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang R, Rosenberg SA,
                        Human NY ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200155393-A2
                                                                                                                                                                                                                                                               immunotherapy
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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Query Match
100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

1 GAARASGPGGGAPR 14 |||||||||||| 49 GAARASGPGGGAPR 62

ሯ

Db 49 GAARASGPGGGAPR 62 Search completed: March 13, 2006, 19:03:59

Job time : 105.412 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24; Search time 16.6353 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-27 74 1 GAARASGPGGGAPR 14 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 80:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР				
Result No.	Score	Query Match	Length	DB	D	Description
-	50	67.6	82	2	T04476	acclimation protei
7	49	66.2	222	~	T36115	probable oxidoredu
9	48	64.9		~	S50754	hypothetical prote
4	48	64.9		~	T35694	ATP dependent DNA
S	45	60.8		~	AB3648	flagellar basal-bo
9	44.5	60.1		~	T21096	hypothetical prote
7	44.5	60.1		~	T21095	
ω	44.5	60.1		N	A36226	.5
σ	44	σ		~	E72464	hypothetical prote
10	44	σ		7	A47008	
11	44	σ		~	S04673	H+-transporting tw
12	44	59.5			A48082	MAP kinase 3 (EC 2
13	44	59.6		~	B70694	probable infB - My
14	44	59.5		7	F87103	initiation factor
15	44	σ	113	~	A41350	adenylate cyclase
16	44	59.5	319	~	T13828	CREB-binding prote
17	43	58.1	185	~	T36874	
18	43	58.1	18	7	AE3136	
19	43	58.1	18	~	G98151	hypothetical prote
20	43	58.1		N	S42585	w
21	43	58.1	N	N	T32525	hypothetical prote
22	43	58.1		N	B72677	
23	43	58.1	m	~	S55626	hypothetical prote
24	43	58.1		~	S28184	_
25	43	58.1	380	7	JC1451	Ca2+/calmodulin-de
56	43	58.1		7	137405	polypeptide N-acet
27	43	58.1	627	7	T35608	polyketide hydroxy
28	43	58.1	9	~	S02165	regulatory protein
53	43	58.1	954	~	A87431	regulatory protein

DNA-binding protei	nitrogen regulator	hypothetical glyci	ovo protein - frui	peptidyl-tRNA hydr	conserved hypothet	hypothetical prote	FRAT2 protein - hu	tail fiber protein	hypothetical prote	homeotic protein e	myristylated alani	aldose 1-epimerase	endopeptidase Clp	hypothetical prote	conserved hypothet
A56038	A34755	B70807	S16356	H87399	G75519	G72663	JC7618	TLBP2X	T29031	C48423	S08341	C87425	T52451	T15143	T36104
0	-	N	N	7	N	N	~	٦	N	~	~	~	7	~	7
1028	1036	1079	1213	143	166	201	233	266	327	333	335	378	387	435	436
58.1	58.1	58.1	58.1	8.95	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8
43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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A,Cross-references: UNIPROT:Q40033, UNIPARC:UPI00009CE5A, EMBL:X97917; NID:g1418969; P A,Experimental source: cv. Igri
C,Genetics:
A,Gene: blt14.2
                           C;Species: Hordeum vulgare (Darley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Datesion: TQ476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Plant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRNA stability and localisation of the low temperature responsive barley gene A;Title: mRNA stability and localisation of the low temperature responsive barley gene A;Reference number: Z1S367; MUID:97299834; PMID:9154983
A;Accession: T04476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%;
acclimation protein 2 - barley
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-82 <PHI>
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Gaps ö 3; Indels Score 50; DB 2 Pred. No. 4.5; 1; Mismatches Query Match
Best Local Similarity 69.2%

1 GAARASGPGGGAP 13 셤 ઠે

31 GAARGAGAGGGVP 43

probable oxidoreductase - Streptomyces coelicolor

C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004 R; Murphy, L; Harris, D; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Sy Reference number: 221597 A; Reference number: 221597 A; Reference number: DNA A; Residues: 1-222
A; Residues: 1-222
A; Residues: UNIPROT: 09X887; UNIPARC: UP10000DB008; EMBL: AL049707; PIDN: CAB41281 A; Experimental source: strain A3(2) C; Genetics:
A; Cenerics: Cenerics: A; Cenerics: Cen

ö Gaps ó, Score 49; DB 2; Length 222; Pred. No. 14; 1; Mismatches 3; Indels Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative

1 GAARASGPGGGAP 13

Gaps

. 0

Length 173;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-692 <MIL>
A;Residues: U-692 <MIL>
A;Cross-references: UNIPROT:Q19579; UNIPARC:UPI000079A30; EMBL:Z50110; PIDN:CAA90444.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-566 <WIL>
A,Cross-references: UNIPROT:Q19581; UNIPARC:UP10000079311; EMBL:Z50110; PIDN:CAA90446.1
A,Experimental source: clone F18H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Map position: X
A,Introns: 111/1, 215/2; 469/3; 552/3
C,Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: X
A,Introns: 111/1; 215/2; 469/3; 552/3
C,Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F18H3.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T21095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.1%; Score 44.5; DB 2;
62.5%; Pred. No. 1.2e+02;
vative 0; Mismatches 3;
                                                                                                                                                        60.8%; Score 45; DB 2;
64.3%; Pred. No. 37;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Reference number: Z19373
A, Accession: T21096
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R, Coles, L. submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted to the EMBL Data Library, July 1995 A; Reference number: Z19373 A; Accession: T21095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 GAPRVGGPGVQMGGAP 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAARASGPG---GGAP 13
                                                                                                                                                                                                                                                                                                                                                                                                   125 GAPIVLNÞGGGAÞR 138
                                                                                                                                                                                                                                                                                                                         1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                               Conservative
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                                                                                                                   Query Match
Best Local Similarity
Local 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Genetics:
A, Gene: CESP: F18H3.3b
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    C;Genetics:
A;Gene: BMEII1107
A;Map position: II
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                                                                                                                                                                                                                                                                       C;Species: Chlanydomonas eugametos
C;Species: Chlanydomonas eugametos
C;Date: 14-Uul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
C;Accession: S50754
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754
A;Reference number: S50754
A;Accession: S50754
A;Mulcoule type: mRNA
A;Molecule type: mRNA
A;Reference number: University
A;Molecule type: mRNA
A;Reference number: NA
A;Coss-references: UNIPROT: Q39492; UNIPARC: UPI00000A170A; EMBL: L29028; NID: 9530877; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T35694
R; Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submiris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submiris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A; Reference number: Z21587
A; Rocession: T35694
A; Accession: T35694
A; Accession: T35694
A; Roceule type: DNA
A; Roceule type: A; Roce
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Cispace: Ol-Reb-2002 #sequence_revision Ol-Reb-2002 #text_change 09-Jul-2004
Cispace: Ol-Reb-2002 #sequence_revision Ol-Reb-2002 #text_change 09-Jul-2004
Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: AB3648
A, Status: preliminary
A, Molecule type: DNA
A, Rosedues: 1-173 «KUR»
A, Ross - references: UNIPROT: 08YAZ4; UNIPARC: UPI0000058740; GB: AE008918; PIDN: AAL54349.1;
A, Experimental source: strain 16M
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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64.3%; Pred. No. 99;
ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
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Pred. No. 27;
                                                                                                                                                                                                                                          hypothetical protein WP6 - Chlamydomonas eugametos
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1437 GSANGSGPEGSAPR 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
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|:|||||| | |
181 GSARASGPSAGRP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 dspraspeddepp 308
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Best Local Similarity 64.37
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A;Cross-references: UNIPROT:P49716; UNIPARC:UP100001274A2; GB:S63168; NID:g386449; PIDN A;Experimental source: prostate carcinoma cell line LNCaP A;Note: sequence extracted from NCBI backbone (NCBIN:134356, NCBIP:134357)
                                                                                       Rikinoshita, S.; Akira, S.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 1473-1476, 1992
A;Title: A member of the C/EBP family. NF-II6 beta, forms a heterodimer and transcripti A;Reference number: A40225; MUID:92159071; PMID:1741402
                                                                                                                                                                                                                                                                            A;Residues: 1,'T',3-12,'G',14-269 <KIN>
A;Cross-references: UNIPARC:UP10000053FFB; GB:M83667; NID:g189175; PIDN:AAA59927.1; PID
A;Note: sequence extracted from NCBI backbone (NCBIN:82662, NCBIP:82663)
                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: GDB:CEBPD; CRP3; CELF
A,Cross-references: GDB:132661; OMIM:116898
A,Map position: 8q11-8q11
C,Superfamily: CCAAT/enhancer-binding protein alpha
C,Superfamily: CCAAT/enhancer-binding protein alpha
C,Keywords: leucine zipper; transcription regulation
F;226-254/Region: leucine zipper motif
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MAP kinase 3 (EC 2.7.1.-) - human
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Local Similarity 64.3%;
les 9; Conservative
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A;Molecule type: mRNA
A;Residues: 1-379 <CHA>
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Les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: E72464
R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jamazaki, J.; R
DNA, Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz
A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                              C;Accession: A36226
R;D'Alession: A36226
R;D'Alessio, M.; Ramirez, F.; Suzuki, H.R.; Solursh, M.; Gambino, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 9303-9307, 1989
A;Title: Structure and developmental expression of a sea urchin fibrillar collagen gene. A;Reference number: A36226; MUID:90083256; PMID:2594770
A;Accession: A36226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription activator NF-IL6 beta - human
N;Alternate names: d(CCAAT)-enhancer-binding protein delta, (C/EBP delta); transcription
C;Species: Home sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47008; A40225
E;Accession: A47008; A40225
B;Cleutjens, C.B.; van Bekelen, C.C.; van Dekken, H.; Smit, E.M.; Hagemeijer, A.; Wagner
A;Title: The human C/EBP delta (CRP3/CELF) gene: structure and chromosomal localization.
A;Reference number: A47008; MUID:93300531; PMID:8314590
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A;Molecule type: DNA
A;Residues: 1-220 <KAW>
A;Cross-references: UNIPROT:Q9Y9C7; UNIPARC:UP1000005E2F9; DDBJ:AP000064; NID:G5105945;
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                      collagen alpha 1 chain - sea urchin (Paracentrotus lividus)
C;Species: Paracentrotus lividus (common urchin)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 С'Species: Aeropyrum pernix
C'Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels E
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A;Gene: APE2360
C;Superfamily: Aeropyrum pernix hypothetical protein APE2360
C;Superfamily: Aeropyrum pernix hypothetical protein APE2360
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Pred. No. 62;
2; Mismatches
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61.1%;
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ilarity 57.1%;
Conservative
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182 GATRVARPGGGSDR 195
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Best Local Similarity 61.1%
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-730 <DAA>
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A;Molecule type: DNA
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H++transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica C;Species: Rhodopseudomonas blastica C;Species: Rhodopseudomonas blastica C;Species: 07-Sep-1990 #text_change 31-Dec-2004 C;Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004 C;Accession. S.04673 W.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Tritle: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription. A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status; not compared with conceptual translation
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(Species: Homo sapiens (man)
(Species: Homo sapiens (man)
(Species: Homo sapiens (man)
(Species: Man)
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A;Cross-references: UNIPROT:P05436; UNIPARC:UP10000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Reywords: ATP biosynthesis; hydrolase; membrane-associated complex
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       Length 269;
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69.2%; Pred. No. 77;
cive 1; Mismatches
Score 44; DB 2
Pred. No. 73;
0; Mismatches
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59.5%;
           59.5%;
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                                                                    GAARASGPGGGAPR 14
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Best Local Similarity 80.0-
           Query Match 59.5
Best Local Similarity 71.4
Matches 10; Conservative
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Job time: 16.6353 secs
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A,Status: preliminary
A,Molecule type: DNA
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A;Reference number: $23426; MUID:92316223; PMID:1319925
A;Accession: $23428
A;Molecule type: mRNA
A;Residues: 25-173,'1',175-379 <GON>
A;Cross-references: UNIPARC:UPI000016A2B4; EMBL:Z11696; NID:923882; PIDN:CAA77754.1; PIL
A; Experimental source: hopatoma cell line HEP G2.

A; Experimental source: hepatoma cell line HEP G2.

A; Note: authors translated the codon AGC for residue 174 as 11e

E; Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.

Bjochem. Biophys. Res. Commun. 182, 1146-1422, 1992

A; Pitle: Extracellular signal-regulated kinases in T cells: characterization of human ER A; Reference number: JQ1400; MUID:92171961; PMID:1540184

A; Accession: POG270

A; Molecule type: mRNA

A; Residues: 14-173, 'I', 175-379 < OWA>

A; Residues: 14-173, 'I', 175-379 < OWA>

A; Experimental source: cell line CBM

B; GD02alez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.

BESS Lett. 334, 170-178, 1992
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Best Local Similarity 69.2
Matches 9; Conservative
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initiation factor IF-2 [imported] - Mycobacterium leprae
[Species: Rathor 103]
[Species: Ryllor 103]
[Species: Mycobacterium leproy
[Mycobacterium leproy
[Myc
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R;Krupinski, J.; Coussen, F.; Bakalyar, H.A.; Tang, W.J.; Feinstein, P.G.; Orth, K.; Sla
Science 244, 1558-1564, 1989
A;Title: Adenylyl cyclase amino acid sequence: possible channel- or transporter-like str
A;Reference number: A41350; MUID:89298382; PMID:2472670
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A;Molecule type: mRNA
A;Residues: 1-1134 <KKU>A;Residues: 1-1134 <KKU>A;Cross-references: UNIPROT:P19754; UNIPARC:UPI000112886C; GB:M25579; NID:g162612; PIDN
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A;Cross-references: UNIPROT:Q9Z519; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g13093370;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
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Pred. No. 2.4e+02;
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DB 2;
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oryza sativ homo sapien xanthomonas

anaeromyxob magnaporthe

Run

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Q7QEK5_ANOGA
Q4RDF1_TETNQ
Q63KC9_BURPS
Q62BA7_BURPS
Q81519_ORYSA
Q52BE2_ORYSA
Q52BE2_ORYSA
Q7F1E3_ORYSA
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Homo sapiens (Human).
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15-DEC-1998 (Rel. 37, Last seq
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                                                                                                            March 13, 2006, 18:53:23 ; Search time 101.624 Seconds (without alignments) 97.196 Million cell updates/sec
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
H. testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lethe B.G.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
                                                                                                     Last sequence update)
Last annotation update)
142 AA
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                                                                                                                                                                           (Fragment)
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unexpected translation product of LAGE-1.";
Int. J. Cancer 82:442-448 (1999).
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                                                                                                                                                                                                                           Flatzer M.;
Submitted (JUL-2001)
                                                                                                                                                                          [4]
NUCLEOTIDE SEQUENCE.
                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                               Platzer M
                                                                                                                                                                                                                     Platzer M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                              MEDLINE-98289662; PubMed-9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen B., Boon T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                            WUCLEOTIDE SEQUENCE.
MEDLINE=98430682; bubMed=9759882;
MEDLINE=98430682; bubMed=9759882;
Schwartzentruber D.J., Rosenberg S.A.;
"A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames.";
J. Immunol. 161:3596-3606(1998).
-!- TISSUE SPECIPTCITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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MEDLINE=21566154; Pubmed=11709543; DOI=10.1093/hmg/10.22.2557;
Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 74; DB 1; Length 180; 100.0%; Pred. No. 0.031;
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; B122C5C2C8BE1569 CRC64;
  Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
                                                                                                                                                 "LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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EMBL; AJ003149; CAA05908.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
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                                          NUCLEOTIDE SEQUENCE
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Matches
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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDINES9954989; PubMed=10523621;
MEDINES9954989; PubMed=10523621;
MEDINES9954989; PubMed=10523621;
Die Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
Die Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
The and tumor specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lethe B., Iucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T.; "LAGE-1, a new gene with tumor specificity."; Int. J. Cancer 76:903-908(1998).
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   a 35
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"Multiple pathogenic and benign genomic rearrangements occur at kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.031;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF277315; AAL27014.1; -; Genomic_DNA.
EMBL, A275977; CAB76943.1; -; Genomic_DNA.
EMBL, AF277315; AAL27013.1; -; Genomic_DNA.
SEQUENCE 180 AA; 17992 MW; B122C5CZC8BE1569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                           Platzer M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
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MEDLINE=98289662; PubMed=9626360;
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Matches
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                         TISSUE=Placenta;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

W. Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Rausner R.D. Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Boares M.B., Medin T.B., Toshiyuki S., Carninci P., Prange C.,

Rahls S.S., Logdellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.M., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Mysrs R.M.,

Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Poly-Pro.
MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
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LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                   Name=LAGE-1B; Synonyme=LAGE-1L;
ISOId=075638-1; Sequence=Displayed;
Name=LAGE-1A, Synonyme=LAGE-1L;
ISOId=075638-2; Sequence=VSP_004301;
ISOId=075638-2; Sequence=VSP_004301;
-!- TISSUE SPECIFICITY: Testis and very low level in placenta and in some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: A transmembrane domain is present in isoform LAGE-1A. SIMILARITY: Belongs to the CTAG family.
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Pred. No. 0.42;
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                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
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/FTId=VAR_007856.
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/FTId=VAR_007855.
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/FTId=VAR 007857
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EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL; AJ223040; CAA11043.1; -; mRNA.
EMBL; AJ223041; CAA11044.1; -; mRNA.
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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188
210
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BC002833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
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Burkholderiaceae, Burkholderia.
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PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.0%; Score 54; DB 2; Length 362; 83.3%; Pred. No. 28; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=BPSL2936;
Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerase III, delta subunit (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=holA; OrderedLocusNames=BMA2451;
Burkholderia mallei (Pseudomonas mallei)
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, 1
Putative DNA polymerase III.
                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
14
                                                                49 GAARASGPRGGAPR 62
                                                                                                                                                                                                                                   Q63QT8_BURPS PRELIMINARY;
Q63QT8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q62H22 BURMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 ARAAGPGGDAPR 359
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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1; Indels

Pred. No. 0.42 0; Mismatches

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SEQUENCE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
Hum. Mo G. Genet. 10:339-352(2001).
EMBL, AE006463, AAK61225.1; -; Genomic_DNA.
Ensembl; RSSG0000167933; Homo sapiens.
SEQUENCE 321 AA; 32979 MW, 9C8764CFA17P4CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
Structural flexibility in the Burkholderia mallei genome.";
Froc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
TIGR: BMA2251;
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                                                                                                                                                                                                                 GO, GO:0003887, F:DNA-directed DNA polymerase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR010372; DNA pol3 delta.
InterPro; IPR05999; DNA pol1II delta.
Ffam; PF06144; DNA pol3 delta; I.
TIGREMMS; TIGR01128; holA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%; Score 54; DB 2; Length 362; 83.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 2; Length 321;
Pred. No. 46;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                   Complete proteome, Nucleotidyltransferase, Transferase. SEQUENCE 362 AA; 38726 MW, D5FF3DE783D41E41 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96527_HUMAN PRELIMINARY; PRT; 321 AA.
Q96327;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gene X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 AA
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76.9%;
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QGGRAB;
01-MAR-2001 (TEMBLEB1 16,
01-MAR-2004 (TEMBLEB1 16,
01-MAR-2004 (TEMBLEB1 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 ARAAGPGGDAPR 359
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Best Local Similarity 76.9'
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5 AARRAGPGGGAAR 17
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Matches 10; Conservative
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Q9GRAB_GR
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Chao Y.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chao Y.-T., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Hsiung J.-M., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Ii Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
"Oryza sativa BAC OSJNBD0012G1 genomic sequence.";
Submitted (SEP-2004) to the EMBL/Genbank/DDBJ databases.

EMBL, AC135421, AAU10755.1; -; Genomic_DNA.
Hedgehog protein (Fragment).
Gryllus bimaculatus (Two-spotted cricket).
Ebkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
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                                                                                                                                                                                                                                                 MEDLINE=20461145; PubMed=11003837; Misumi Y., Ohuchi H., Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H., Yoshioka H., Noji S.; "Correlation of diversity of leg morphology in Gryllus bimaculatus (cricket) with divergence in dpp expression pattern during leg
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza
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R GO; GO: 0007267; P: cell-cell signaling; IEA.

R GO; GO: 0007275; P: cell-cell signaling; IEA.

R GO; GO: 00016539; P: intein-mediated protein splicing; IEA.

R GO; GO: 0006508; P: proteolysis and peptidolysis; IEA.

R InterPro; IPR003586; Hedgehog_hint_C.

R InterPro; IPR003279; Hedgehog_hint_N.

R InterPro; IPR000320; HH signal.

R InterPro; IPR001617; Peptidase C46.

InterPro; IPR001767; Peptidase C46.

R Pfam; PF01085; HH signal; I.

R Pfam; PF01087; HH signal; I.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein OSJNBb0012G21.2
Name=OSJNBb0012G21.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Development 127:4373-4381(2000).
EMBL, AB044709; BAB19658.1; -; mRNA.
HSSP; Q62226; 1VHH.
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SMART; SM00305; HintC; 1.
SMART; SM00306; HintN; 1.
PROSITE; PS50817; INTEIN_N_TER; 1.
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78.6%; Pred
0; 1
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QGBBJS ORYSA PRELIMINARY;
QGBBJS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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MEROPS; C46.001; -.
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                                                                                                                                                           NCBI_TaxID=6999;
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Hypothetical
SEQUENCE 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAMEDLINE-21638749; PubMed=11780052; DOI=10.1038/4148658;
RA MEDLINE-21638749; PubMed=11780052; DOI=10.1038/4148658;
RA MEDLINE-21638749; PubMed=11780052; DOI=10.1038/4148658;
RA Deloukas P., Matthews L.H., Abhurst J.L., Burton J., Gilbert J.G.R.,
RA Bailey J., Barlow K.P., Bates K.N., Barden A.M., Brown A.J.,
RA Basaley O.P., Bird C.P., Blakey S.E., Baridgeman A.M., Brown A.J.,
RA Clegg S., Cobley V.E., Collier R.E., Cornor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Gollier R.E., Connor R.E., Corby N.R.,
RA Hungton A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Huntele E., Hunt A.R., Hunt A.R., Hanley D., Holden J.L., Howden P.J.,
RAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RAY M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RAY M.P., Mistry D., McConnachie L.J., McLay K., McMarray A.A.,
MILL S.L., Mistry D., McConnachie L.J., McCay K., McMarray A.A.,
RA RA, R., Ray R., Batel R., Bearce T.A.V., Peck A.I.,
RA RILL S.L., Ross M.T., Soderlund C., Schward C.A., Sulston J.E.,
RA Shuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA RILL R.M., Tromans A.C., Vaudin M., Wall M., Walley D., Williems L., Whittehead S.L., Whittehead S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                            ö
                                                                                                                                                                                        DB 2; Length 644;
              GO; GO:0004057; F:arginyltransferase activity, IEA.
GO; GO:0016598; P:protein arginylation; IEA.
GO; GO:001276; P:regulation of protein catabolism; IEA.
InterPro; IPR007472; ATE C.
InterPro; IPR007471; ATE N.
Pfam; PF04377; ATE C.
Pfam; PF04377; ATE C.
Hypothetical proteIn:
                                                                                                                                                                                                                          1; Indels
                                                                                                                                                     644 AA; 72444 MW; DDB97FC0C40C23F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: Contains 2 ANK repeats.
-i- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-Cthetical protein C20orf86.
                                                                                                                                                                                                                                                                                                                                                                            337 AA
                                                                                                                                                                                                      Pred. No. 88;
0; Mismatches
                                                                                                                                                                                        Score 52;
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                        70.3%;
                                                                                                                                                                     Query Match
Best Local Similarity 90.57
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                               9 GAASASGPGGG 19
                                                                                                                                                                                                                                                        1 GAARASGPGGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Gramene; Q688J5; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                              CTOB6 HUMAN
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The DNA
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                                                                                                                                                                                                                                                                                                                                                          CT086 HUMAN
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   SX DR DR DR DR SX
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein OSJNBa0063118.9.
Name=OSJNBa0063118.9,
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Yaan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vansken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mite O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBa0063118 genomic sequence.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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0
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Pred. No. 66;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 2; Length 367;
Pred. No. 71;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases EMBL, AC107206; AAT77052.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                 ANK repeat, Hypothetical protein, Polymorphism, Repeat DOMAIN 88 164 Ubiquitin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il protein.
367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          R -> C (in dbSNP:584855).
/FTId=VAR 014400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EC8BA4AD414756CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 AA.
                                          Ensembl; ENSG0000124227; Homo sapiens.
HGNC; HGNC:16217; C20orf86.
InterPro; IPR00210; ANK.
InterPro; IPR00210; ANK.
INTERPRO; IPR00216; Ubiquitin.
Pfam; PF00023; ANK; 2.
PRINTS; PR01415; ANKYRIN.
SMART; SN00248; ANK; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50089; ANK_REP_REGION; 1.
PROSITE; PS00299; UBIQUITIN 1; FALSE_NEG.
PROSITE; PS00293; UBIQUITIN 1; FALSE_NEG.
EMBL; AL354776; CAC17565.2; -; Genomic_DNA.
HSSP; P42771; 2A5E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                         ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 AA; 36714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%;
76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.40,
Best Local Similarity 71.40,
To 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |||:|| ||| ||
9 GGARAAGPTGGASR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AAAASGPGGGSAR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEAV33 ORYSA PRELIMINARY;
QEAV33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 76.9
Watches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=39947;
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RESULT 12

Gaps

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Hordeum vulgare (Barley).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Pissipedia; Canidae;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97299834; PubMed=9154983; DOI=10.1023/A:1005717613224; Phillips J.R., Dunn M.A., Hughes M.A.; Phillips J.R., Dunn M.A., Hughes M.A.; Mannaka stability and localisation of the low temperature responsive barley gene family blil. 1997). Plant Mol. Biol. 33:1013-1023(1997). Plant Mol. Biol. 33:1013-1023(1997). Plant Mol. Biol. 34:1013-1023(1997). Plant Mol. Biol. 34:1013-1023(1997). Second Seco
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.9%; Score 51; DB 2; Length 867; 64.3%; Pred. No. 1.6e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 2; Length 82;
Pred. No. 24;
1; Mismatches 3; Indels
                                                                                                                                                                                                  Buell R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein.
867 AA; 92812 MW; 7365009715EDDC21 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Pancreatic duodenal homeobox gene 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA
                                                                                                                                                                                                                                                                             EMBL; AC084404; AAK50601.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                         Gramens, Q94LD1; -.
InterPro; IPR007228; DUF390.
InterPro; IPR007321; Transposase_28.
Pfam; PF04194; DUF390; 3.
Pfam; PF04195; Transposase_28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 GGSRAGGPGGGGSR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAARASGPGGGAPR 14
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QSNTAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q40033 HORVU PRELIMINARY;
Q40033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.4.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAARASGPGGGAP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                              NUCLEOTIDE SEQUENCE
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Name=blt14.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Doverton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J., Yuan Q.;
databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buell R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-DFB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein OSMBa0011L09.12.
ORFNames=OSJNBa0011L09.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OSJNBa0026A15.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell C.R., Wing R.A., McCombie W.R., Messing Submitted (MAX-2003) to the EMBL/GenBank/DDBJ EMBL, AC092388; AAM22719.1; -; Genomic_DNA. EMBL, AE017090; AAP53592.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 867 AA
                                               559 AA
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InterPro; IPR007321; Transposase_28.
Pfam; PF04094; DUF390; 2.
Pfam; PF04195; Transposase_28; 1.
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nes 9; Conservative
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Q94LD1 ORYSA PRELIMINARY;
Q94LD1;
       10 ORYSA
QBL680 ORYSA PRELIMINARY;
Q8L680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
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RESULT 13 Q94LD1_ORY

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P NUCLECTIDE SEQUENCE.

A Takagi K., Neo S., Furuichi M., Watanabe M., Kansaku N., Hisasue M.,

A Takagi K., Neo S., Furuichi M., Watanabe M., Kansaku N., Hisasue M.,

A Tacaine Pdx-1.", Yamada T.;

Canine Pdx-1.", Tonine Pdx-1.", 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 13, 2006, 19:14:27 Job time : 102.624 secs
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15 GGSRASSPGGAQPR 28
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Sequence 25611, A Sequence 21, Appl Sequence 2710, A Sequence 2942, A Sequence 2942, A Sequence 1930, A Sequence 26, Appl Sequence 26, Appl

Sequence 16943, A Sequence 23, Appl

Sequence Sequence Sequence

OM protein

Run on:

Sequence:

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100.0%; Score 74; DB 1; Length 180; 100.0%; Pred. No. 0.025; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COMPRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
COMPUTER: BY PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
US-10-104-047-3295
US-09-902-540-13196
US-09-252-911A-2511
US-09-252-911A-26110
US-09-252-911A-29442
US-09-252-991A-19951
US-09-252-991A-19951
US-09-252-991A-19951
US-09-252-991A-19951
US-08-333-5-66-26
US-08-333-5-66-26
US-08-945-118-26
US-09-945-118-26
US-09-945-118-26
US-09-952-991A-27111
US-09-252-991A-27111
US-09-252-991A-25927
US-09-252-991A-15943
US-08-252-991A-15943
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
ATTLE OF INVENTION: L1
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
STRRESSEE: Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston
                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                          ; Sequence 9, Application US/08791495; Patent No. 5811519; Patent No. 7811519; ARPENEAL INFORMATION: APPLICANT: Leth, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 GAARASGPGGGAPR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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1134
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 FILING DATE:
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US-08-791-495-9
 US-08-791-495-9
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Sequence 30219, A
Sequence 117, App
Sequence 117, App
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Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 17335, A
Sequence 17249, A
Sequence 10, Appli
Sequence 7, Appli
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Sequence 19752, 7
Sequence 32326, 7
Sequence 31759, A
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Sequence 31279,
Sequence 23998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                       March 13, 2006, 19:14:49 ; Search time 26.0235 Seconds (without alignments) 44.477 Million cell updates/sec
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Sequence 25, A
Sequence 15, A
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            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                          1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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US-09-751-796-8

US-09-341-829A-9

US-09-341-829A-9

US-09-341-829A-9

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-252-991A-1735

US-09-252-991A-17249

US-09-252-991A-17249

US-09-252-991A-17249

US-09-252-991A-17249

US-09-323-91A-17249

US-09-323-91A-17249

US-09-323-91A-17249

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US-09-323-91A-30219

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US-09-252-991A-30527

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US-09-252-991A-31279
US-09-252-991A-23998
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                       1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
                                                                                                                                             US-09-529-206E-27
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Match Length DB
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899.2
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Perfect score:
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47.5
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Result No.

Minimum DB Maximum DB

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US-09-392-714-25
COUNTRY:
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                                                                                 Sequence 8, Application US/08937263B
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Jager, Elke;
dapplicant: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ITSELF, AND USES THEREOF
TITLE OF INVENTION: ITSELF, AND USES THEREOF
TITLE OF INVENTION: ITSELF, AND USES THEREOF
CORRESPONDENCE ADDRESS:
GORRESPONDENCE ADDRESS:
STREET: 666 Fifth Avenue
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
STATE: New York
COUNTRY: Light Avenue
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
   APPLICANT: Stockert, Elisabeth, Jager, Elke;
   APPLICANT: Then, Yao-tseng; Scanlan, Matthew;
   APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
   APPLICANT: Knuth, Alexander; Old, Lloyd J.
   TITLE OF INVENTION: Antibodies Which Bland to NY-ESO-1 Cancer;
   TITLE OF INVENTION: Truncated Proteins, Uses Thereof;
   TITLE OF INVENTION: Binding Peptides Derived Therefrom
   NUMBER OF SEQUENCES:
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Fulbright & Jaworski, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 74; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 0.025; Matches 14; Conservative 0; Mismatches 0; Indels
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STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

SOFTWARE: Wordberfect

CURRENT APPLICATION DATA:

PRICE SPELICATION DATA:

PRICE APPLICATION NUMBER: US/08/937,263B

FILING DATE: September 15, 1997

PRIOR APPLICATION NUMBER: 08/725,182

FILING DATE: October 3, 1996

ATTORNEY/AGRYT INFORWATION:

NAME: Sinn, Eric, Patent Agent

REGISTRATION NUMBER: 40,177

REFERENCS/DOCKET NUMBER: 40,177

REFERENCS/DOCKET NUMBER: 40,177

REFERENCS/DOCKET NUMBER: 1UD 5466.1

TELECOMMUNICATION INFORMATION:

TELEFHONE: (212) 318-3000

TELEFHONE: (212) 318-3000

TELEFANCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-937-263B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Guze, All O.
APPLICANT: Guze, All O.
APPLICANT: Guze, All O.
APPLICANT: Guze, All O.
APPLICANT: Glas, D.
APPLICANT: Clan, Yao-Tseng
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses;
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE REPRESENCE: L0461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT APPLICATION NUMBER: PCT/US98/14679
EARLIER APPLICATION NUMBER: PCT/US98/14679
SOFTWARE: FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: RT
COUNTYER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                       OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 3996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1010 5466.3
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 318-3168
TELEFRAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAARASGPGGGAPR 14
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Best Local Similarity 100.
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US-09-392-714-25
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    <151> 1998-01-27
                                                                                                                                                                                                      100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.025;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESSEDONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-849-602-30
Sequence 30, Application US/09849602
Sequence 30, Application US/09849602
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel;
FILE REFERENCE: LO461/7105(JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 74; DB 2; 100.0%; Pred. No. 0.025;
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                                                                                                                                                                                                                                                  Mismatches
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PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08791495
Patent No. 5811519
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                          1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                  14; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-341-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                          LENGTH:
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                                                                                                      APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Patent No. 6794131

GENERAL INFORMATION:
APPLICANT: Leth., Bernard
APPLICANT: Leth., Bernard
APPLICANT: Locas, Sophie
APPLICANT: Godelaine, Daniels
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERRENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT APPLICATION NUMBER: US/09/341,495
PRIOR APPLICATION NUMBER: US 08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811) TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILLING DATE: 02-0ct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08/977,263
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6723832man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear;
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,946
                                     Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 180 amino acids TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 GAARASGPGGGAPR 62
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                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: USA
                       US-09-165-546D-15
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Wolf, Greenfield & Sacks, P.C.

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ADDRESSEE:
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LENGTH: 210
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APPLICANT: Leth, Bernard

APPLICANT: Lucas, Sophie

APPLICANT: Description:

APPLICANT: Description:

APPLICANT: Description: Daniele

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS

FILE REFRENCE: L0461/7066

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US 09/791,495

PRIOR APPLICATION NUMBER: DCT/US98/01445

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for windows Version 3.0

SEQ ID NO 7

LEMOTH: 180
                                                                                                                                                                                                                                                                                                                                                                              Query Match

89.2%; Score 66; DB 1; Length 180;
Best Local Similarity 92.9%; Pred. No. 0.25;
Matches 13; Conservative 0; Mismatches 1; Indels
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| Patent No. 5811519
| GENERAL INFORMATION:
| APPLICANT: Leth, Bernard
| APPLICANT: Locas, Sophie
| APPLICANT: De Smet, Charles
| APPLICANT: Boon-Falleur, Thierry
| TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS:
  PILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Van Amsteredam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUINTATION INFORMATION:
TELEFAX: 617-720-2441
INFORMATION POR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLLGY: linear
TOPOLLGY: linear
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09341829A Patent No. 6794131
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                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-791-495-7
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-341-829A-7
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US-08-791-495-5
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; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
   APPLICANT: Lucth,, Bernard
; APPLICANT: Luch, Sophie
; APPLICANT: Lucas, Sophie
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUWOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; NUMBER OF SEQ ID NOS: 14
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Pred. No. 0.28;
0; Mismatches 1; Indels
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Pred. No. 0.28;
0; Mismatches 1; Indels
                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                    L0461/7005
                                                                      COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0463
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPAK: 617-720-3441
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE FRARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acids
TYPE: amino acids
               600 Atlantic Avenue
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Best Local Similarity 92.93
Matches 13; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
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MOLECULE TYPE: protein
US-08-791-495-5
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; ORGANISM: Homo sapiens
US-09-341-829A-5
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STREET: 00...
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                                                                                                                                                                                                           Length 160;
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                                                                                                                                                                                                       Score 50; DB 2;
Pred. No. 22;
                                                                                                                                                                                                                                               1; Mismatches
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  PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17249
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Oregon
COUNTRY: United States of America
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/789,329C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01/23/97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EATP, David J.
REGISTRATION NUMBER: 41,40
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                       67.6%;
69.2%;
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Best Local Similarity 69.2
Matches 9; Conservative
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FILING DATE: 01/23/97
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STRANDEDMESS: single

; TOPOLOGY: linear

US-08-789-329C-10
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; Sequence 24923, Application US/09252991A
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
    APPLICANT: Marc J. Rubenfield et al.
    TITLE OF INVENTION: NUCLEIC CATC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT PELING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR PELICATION NUMBER: US 60/094,190
; PRIOR PILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24923
    Sequence 17335, Application US/09252991A

Patent No. 6551735

Baggence 17335, Application US/09252991A

Patent No. 6551735

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 1999-02-18

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17335
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US-09-252-991A-17249
Sequence 17249, Application US/09252991A
Setent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
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Pred. No. 16;
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US-09-252-991A-17335
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Best Local Similarity 71.4%;
Matches 10; Conservative
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278 GAGRAAGPGTGQPR 291
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US-09-252-991A-17335
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Search completed: March 13, 2006, 19:18:51 Job time : 27.0235 secs

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Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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Sequence 1404, Application US/10296734

Sequence 1404, Application US/10296734

Publication No. US20040054137A1

GENERAL INPORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor TITLE OF INVENTION: Synthetic molecules and uses therefor CURRENT FILING DATE: 2003-08-04

PRIOR PEPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 74; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 14; Conservative 0; Mismatches 0; Indels
         US-10-295-027-388
US-10-186-832-141
US-10-146-473-69
US-10-146-473-69
US-10-296-734-834
US-10-657-022-75
US-10-657-022-75
US-11-067-064-75
US-11-067-159-75
US-10-17-937-76
US-10-657-022-76
US-10-657-022-76
US-11-067-064-76
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US-10-422
Sequence 202, Application US/10482029
Fublication No. US20050037445A1
GENERAL INFORMATION:
APPLICANT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REFERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Patentin version 3.1
SEQ ID NO 202
                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: NYSOla segment 4 US-10-296-734-1404
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US-10-482-029-202
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   US-10-296-734-1404
 В
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Sequence 202, App
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                                                                                                                        (without alignments)
69.096 Million cell updates/sec
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Sequence 3, 1
Sequence 3, A
Sequence 5024
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Sequence 30,
Sequence 8,
                                                                                                    March 13, 2006, 19:51:56; Search time 84.6588 Seconds
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-482-029-202
US-09-871-798
US-09-871-798
US-10-023-182-8
US-10-207-655-71
US-10-206-33-182-8
US-10-206-33-182-8
US-10-10-10-144
US-10-296-066-3
US-10-10-10-148-32-139
US-10-296-734-832
US-10-296-734-832
US-10-188-32-139
US-10-751-088-15
US-10-751-088-15
US-10-877-373-9
US-10-875-508-3
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US-09-821-883-27
US-11-144-912-27
US-10-296-734-1454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA_Main: *
                                                                                                                                                                                                                                                                            1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                               US-09-529-206E-27
74
1 GAARASGPGGGAPR 14
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Maximum DB seq length: 200000000
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Match Length DB
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100.0
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Score

Result No.

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Gaps

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Stockert, Elisabeth
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US-10-023-182-8
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Patent No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 74; DB 3; Length 180; Pred. No. 0.14; 0; Mismatches 0; Indels
Query Match 100.0%; Score 74; DB 5; Length 179; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 14; Conservative 0; Mismatches 0; Indels
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION 1872-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
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APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                       49 GAARASGPGGGAPR 62
                                                                                              1 GAARASGPGGGAPR 14
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APPLICANT: Scanlan, Matthew J. APPLICANT: Old, Lloyd J.

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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Xnuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodiaes Which Bind to NY-ESO-1 Cancer;
Truncated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
                                                                                                                                                                                                                                                                                                                                                                                                    ;
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Worderfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/751,798
FILING DATE: OCCODER: 3, 1996
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. US20020164665Alman D.
RECISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 100 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York
CUTY: New York
COUNTRY: USA
APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: LO461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
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                   APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: BRITODE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFERENCE: CTLIMM.21CP1C
CURRENT APPLICATION NUMBER: US/06,066
CURRENT PILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 09/56,066
CURRENT PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/561,57
PRIOR PELING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Publication No. USZO030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: LIU Liping
APPLICANT: LIU Liping
APPLICANT: LIU Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIPM: 027A
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/383,017
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2002-03-07
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 180
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Matches 14; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Sequence 14, Application US/10364614

Sequence 14, Application No. US2030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: Gajatic, Sacha

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

TITLE OF INVENTION: 1200-02-24

CURRENT APPLICATION NUMBER: US/10/364,614

SOFTWARE FILING DATE: 2002-02-13

NUMBER OF SEQ ID 60S: 17

SOFTWARE: Patentin version 3.2

SEQ ID NO 14

LENGTH: 180
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US-10-207-655-71
Sequence 71, Application US/10207655
Sequence 71, Application US/10207655
Publication No. US2003118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hadden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNGCLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT PILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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ch 100.0%; Score 74; DB 4; Length 180; al Similarity 100.0%; Pred. No. 0.14; l4; Conservative 0; Mismatches 0; Indels
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; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
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                                                                                                                     1 GAARASGPGGGAPR 14
                                                                                                                                                                           49 GAARASGPGGGAPR 62
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-207-655-71
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                         Best Local Similarity
Matches 14; Conserva
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LENGTH: 180
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                                                                                                           GURREAL INTOCKARILON:

APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Ginaberg, Wendy M.
APPLICANT: Ginaberg, Wendy M.
APPLICANT: Ginaberg, Wendy M.
APPLICANT: Ginaberg, Wendy M.
APPLICANT: Mack, David H.
APPLICANT: Macra, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Macra, Peter A.
APPLICANT: Marray, Richard
APPLICANT: Marray, Richard
APPLICANT: Bob Blocechnology, Inc.
TITLE OF INVERTION: Methods of Screening for Modulators of Cancer
TITLE OF INVERTION: Methods of Screening for Modulators of Cancer
TITLE OF INVERTION NUMBER: US 100-09-15
CURREAT APPLICATION NUMBER: US 60/335,394
PRIOR APPLICANTION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-15
PRIOR APPLICANTON NUMBER: US 60/334,333
PRIOR APPLICANTON NUMBER: US 60/334,3376
PRIOR PELING DATE: 2001-12-14
PRIOR PILING DATE: 2001-12-14
PRIOR PERIOR PILING DATE: 2001-12-14
PRIOR PERIOR PILING DATE: 2001-12-14
PRIOR PERIOR PILING DATE: 2001-12-14
PRIOR PILING DATE: 2001-12-14
PRIOR PERIOR PAPILICATION NUMBER: US 60/356,714
PRIOR PERIOR APPLICATION DATE: 2001-12-13
PRIOR PERIOR P
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Publication No. US20040054137A1

GENERAL INPORMATION:
APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: AU PQ7761/00

PRIOR PELING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 832
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                      Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-296-734-832
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| Sequence 139, Application US/10188832 |
| Sequence 139, Application US/10188832 |
| Sequence 139, Application No. US2004007695SA1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Mack, David H. |
| APPLICANT: Aziz, Natasha |
| TITLE OF INVENTION: methods of Diagnosis of Bladder Cancer, Compositions |
| TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder |
| TITLE OF INVENTION: Cancer |
| FILE REFERENCE: 018501-002330US |
| CURRENT APPLICATION NUMBER: US 60/3302, 814 |
| PRIOR APPLICATION NUMBER: US 60/310, 099 |
| PRIOR APPLICATION NUMBER: US 60/343, 705 |
| PRIOR APPLICATION NUMBER: US 60/343, 705 |
| PRIOR APPLICATION NUMBER: US 60/343, 705 |
| PRIOR FILING DATE: 2001-11-13 |
| NUMBER OF SEQ ID NOS: 207 |
| SOFTWARE: PATENTIN VET: 2.1
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Sequence 11, Application US/1077063
Publication No. US2004013208BA1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK. 02.2c1
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT FILING DATE: 2004-02-10
PRIOR PILING DATE: 2002-11-07
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                                                                                     ; OTHER INFORMATION: NYNSOla consensus polypeptide US-10-296-734-832
                                                                                                                                                                                                                                                                                                                 1 GAARASGPGGGAPR 14
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ORGANISM: Homo sapiens
TYPE: PRT ORGANISM: Artificial
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US-10-777-053-11
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Gaps
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APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNK.032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: 60/409123
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 13, 2006, 20:02:27
Job time: 85.6588 secs
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; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                     49 GAARASGPGGGAPR
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ORGANISM: Homo sapiens
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Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage compuTER: IBM operate: 0.5 inch, 144 kb storage compuTER: IBM operate: 0.5 inch, 144 kb storage compuTER: IBM operate: 0.5 inch, 144 kb storage compuTER: 0.5 inch, 1675, 0.88

TILING SYSTEM: 0.5 inch, 10.7 inch, 10.7 inch, 10.5 in
                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 74; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SSCTWARE: FastSEQ for Windows Version 4.0
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 15 US-10-751-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
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TYPE: amino acid
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; ORGANISM: Homo Sapien
US-10-777-053-11
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LENGTH: 180
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 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 28, Appl
Sequence 20556, App
Sequence 20334, A
Sequence 22333, A
Sequence 22333, A
Sequence 2235, Ap
Sequence 34, Appl
Sequence 34, Appl
Sequence 38, Appl
Sequence 2265, A
Sequence 1240, Appl
Sequence 1260, Appl
Sequence 1260, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 22661, Appl
Sequence 22661, Appl
Sequence 2261, Appl
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Sequence 19104, A
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             March 13, 2006, 19:54:06; Search time 9.55294 Seconds (without alignments) 40.793 Million cell updates/sec
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                                                                                                                                                                                                                                                                                  Published Applications AA New:*

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3: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW-PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW-PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW-PUB.pep:*
        GenCore version 5.1.7
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US-11-096-568A-20334
US-11-096-568A-22333
US-11-096-568A-22333
US-11-096-568A-22333
US-11-096-568A-23335
US-11-096-568A-23806
US-11-096-568A-23806
US-11-096-568A-23806
US-11-096-568A-23806
US-11-096-568A-22662
US-11-129-143-108
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US-11-129-143-108
US-11-1096-568A-22662
US-11-1096-568A-22662
US-11-1096-568A-22662
US-11-1096-568A-22661
US-11-096-568A-22661
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US-11-096-568A-8816
US-11-096-568A-19104
US-10-892-379-5
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                          1616b7 segs, 27834885 residues
                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                       1 GAARASGPGGGAPR 14
                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                       US-09-529-206E-27
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Match Length
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                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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                                                                Run on:
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No.
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19986, A
19988, A
1998, A
145, App
641, App
4, App
1, App
23045, A
25788, A
211531, A
211530, A
25787, A
21193, A
                                     Sequence Seq
US-11-096-568A-19986
US-11-096-568A-19985
US-11-096-568A-19984
US-11-096-568A-41
US-11-096-568A-41
US-11-096-568A-2208
US-11-096-568A-27638
US-11-096-568A-21195
US-11-096-568A-21195
US-11-096-568A-21195
US-11-096-568A-21195
US-11-096-568A-21195
US-11-096-568A-21195
US-11-096-568A-21193
US-11-096-568A-21193
US-11-129-143-113
US-11-129-143-113
US-11-129-143-113
US-11-1241-38-47-88
US-11-1241-38-48-110
   306
3104
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US-11-021-441-28

US-11-021-441-28

Sequence 28, Application US/11021441

Publication No. US20050249748A1

GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DUKETY, William S., Jr.
APPLICANT: COCK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: US/11/021,441

CURRENT APPLICATION NUMBER: US/11/021,441

CURRENT PILING DATE: 2004-12-23

PRIOR FILING DATE: 2004-10-06
113, App
112, App
8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USE
                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/11155288

Publication No. US20060008468A1

GENERAL INFORMATION No. US2006000846BA1

GENERAL INFORMATION: Chih-Sheng

APPLICANT: Chiang, Chih-Sheng

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: ANTIERN IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

FILE REFERENCE: MANNK. 050A

CURRENT APPLICATION NUMBER: 05/500,969

PRIOR APPLICATION NUMBER: 60/580,969

PRIOR APPLICATION NUMBER: 60/580,969

NUMBER OF SEQ ID NOS: 40

SOOTWARE: FREESC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GAARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Sequence 22334, Application US/11096568A

Sequence 22334, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22334
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Sequence 22333, Application US/11096568A

Publication NO. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE REFERENCE: 2750-15920W22

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

LENGTH: 358
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                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                          Score 53; DB 7;
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.6%; Score 53; DB 7; 71.4%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 7;
Pred. No. 3.1;
0; Mismatches
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i LOCATION: (1)...(358)
cother information: Ceres Seq. ID no. 12408543
US-11-096-5688-22333
                                                                                                                                 NAME/KEY: misc_feature
; LOCATION: (1)...(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
i LOCATION: (1).:(353)
cother information: Ceres Seq. ID no. 12408544
US-11-096-5688-22334
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ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                  TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                              71.6%;
76.9%;
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Best Local Similarity 71.4%;
Matches 10; Conservative
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89 GVARADGPGTGAP 101
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity
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                    LENGTH: 306
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US-11-096-568A-20556
US-11-096-568A-20556, Application US/11096568A

| Publication No. US20060048240AI
| Publication No. US20060048240AI
| GENERAL INFORMATION:
| APPLICATION NICKOLAI et al.
| TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
| TITLE REPRENCE: 1760-1592PUS2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 20556
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Sequence 496, Application US/10623155

Publication No. US20050261166A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SOFTWARE FABELICATION WINDOWS VERSION 4.0

SEQ ID NO 496

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 74; DB 7; Length 240; Best Local Similarity 100.0%; Pred. No. 0.0042; Matches 14; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PAPLICATION NUMBER: US 60/599,377
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
TYPE: PRIOR PLAING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PRISEQ for Windows Version 4.0
TYPE: PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-623-155-496
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Sequence 2006, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-15922POS.

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 23806

LENGTH: 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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i LOCATION: (1)...(134)
i THER INDEMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
                                                                                                                                                                                                                                                                                               APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAAA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: MAGHARM: KENJI
APPLICANT: MAGHARM: KENJI
APPLICANT: MAGHARM: KENJI
APPLICANT: MAGHARM: KENJI
APPLICANT: MAGHARM: 000-1 full length cDNA
ITILB OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 0803-0-1
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-0-2
PRIOR FILING DATE: 2001-1-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PARCENT NOS: 4096
SOFTWARE: PARCENT NOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.8%; Score 46.5; D
Best Local Similarity 61.1%; Pred. No. 38;
Matches 11; Conservative 1; Mismatches
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                                             SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                 OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                              IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ARASGPGGGAP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-11-072-512-3295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-096-568A-23806
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                                                                                                                                                                                                  Sequence 22332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERRINCE: 2750-15920422
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10542
LENGTH: 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 420;
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| LOCATION: (1)...(420)
| JOHAR INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332
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LOCATION: (1)..(167)

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US-11-096-568A-10542
  Mismatches
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US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
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                                                                                       112 GAARGOGPGGEOPR 125
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Best Local Similarity 71.45
Matches 10; Conservative
  10; Conservative
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APPLICANT: Nycz, Jeffrey
TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
TITLE OF INVENTION: Osteoinductive Material
FILE REFERENCE: 64118.000087
CURRENT PILLOGATION NUMBER: US/10/921,793
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 830
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TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
TITLE OF INVENTION: Osteoinductive Material
TITLE OF INVENTION: Osteoinductive Material
FILE REFERENCE: 64118.000008;
CURRENT APPLICATION NUMBER: US/10/931,198
CURRENT FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 84
SOFTMARE: PatentIn version 3.2
SOFTMARE: PatentIn version 3.2
LENGTH: 830
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| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Adarmani, Susan
| APPLICANT: Andarmani, Susan
| APPLICANT: Tampy Y. Tom
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: Mubber: US/10/821,234
| CURRENT APPLICATION NUMBER: US/62,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| WINDER OF COLTAN NOT NOT NOT NOT NOT NUMBER: US 60/462,047
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66.7%; Pred. No. 72;
ive 2; Mismatches 2; Indels
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                   Sequence 38, Application US/10921793
Publication No. US20060039949A1
GENERAL INFORMATION:
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SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1240
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673 GSAEAAGPGAGA 684
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673 GSAEAAGPGAGA 684
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Matches 8; Conservative
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US-10-931-198-38
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Best Local Similarity
Matches 8; Conserv
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US-10-921-793-38
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27265
LENGTH: 413
                                                                                                                                                                                                                                                APPLICANT: Magenar, Medissa M.
APPLICANT: Magenar, Medissa M.
APPLICANT: Graziani, Edmund
APPLICANT: Graziani, Edmund
APPLICANT: Summers, Mia
APPLICANT: Summers, Mia
APPLICANT: Nalowski, Kerry
APPLICANT: Pong, Kevin
TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
TITLE OF INVENTION: Dolyketide
FILE REFERENCE: AM-101426US
CURRENT APPLICATION NUMBER: US 60/664,483
FRIOR FILING DATE: 2005-06-03
FRIOR PELLOR DATE: 2005-06-03
FRIOR PILING DATE: 2006-06-03
FRIOR PILING DATE: 2006-06-03
FRIOR APPLICATION NUMBER: US 60/576,895
FRIOR SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34
LENGTH: 280
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Pred. No. 39;
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; LOCATION: (1)...(413)
; OTHER INDEMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265
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                                                                                               Sequence 34, Application US/11143980
Publication No. US20050272133A1
GENERAL INFORMATION:
APPLICANT: He, Min
APPLICANT: Hucul, John
APPLICANT: Hauli, John
APPLICANT: Haltli, Bradley A.
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64.3%;
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61 GVARLAGPGGRAGR 74
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Matches 10; Conservative
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Matches 9; Conservative
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ORGANISM: Streptomyces sp
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RESULT 13

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; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1240
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0; Gaps Query Match 59.5%; Score 44; DB 6; Length 298; Best Local Similarity 64.3%; Pred. No. 39; Matches 9; Conservative 0; Mismatches 5; Indels

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Description	Aay06064 Human can Aay05986 Human can Aay05979 Human can Aay05979 Human can Aay05979 Human can Aaw62584 Cancer a Aaw62584 Cancer a Aaw62656 Human NY- Aay05965 Human can Aay05965 Human can Aay05965 Human can Aay05964 Human NY- Aay07164 Human can Aay07164 Amino aci Aau01535 Human NY- Aau01535 Human NY- Aau01535 Human NY- Aau11543 Human NY- Aau11543 Human NY- Aau11543 Human NY- Aau11543 Human Can Abu56508 Lung canc Abu56508 Lung canc Abu56508 Lung canc Abu56608 Lung canc Abu56608 Lung canc Abu56608 Lung canc Abu56610 Human NY-
SUMMARIES	AAYOGG64 AAYOG986 AAYOG998 AAYOG978 AAYOG979 AAWG5848 AAWG5848 AAWG5848 AAWG5848 AAWG5848 AAWG5848 AARG70862 AAYO1154 AARG7164 AAU11543 AAU11543 ABRS8672 ABRS8672 ABRS86508 ABUS6694 ABUS6694 ABUS6699
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32	89	80	180	œ	ADM72815	Adm72815 Human NY-
33	68	00	180	œ	ADM73418	Adm73418 CAG-3 pro
34	68	90	180	ω	ADM73417	Human
35	89	00	180	æ	ADQ18451	Adq18451 Human sof
36	89	00	180	œ	ADQ10446	Adq10446 Autoimmun
37	89	100.0	180	œ	ADS80926	Ads80926 Tumour as
38	89	100.0	180	σ	ADW44353	Adw44353 Human aut
39	89		180	6	ADY85096	Ady85096 Tumor ant
40	89	•	180	σ	ADZ28913	Adz28913 NY-ESO-1
41	68	100.0	180	σ	ADZ42374	Adz42374 Immunogen
42	68		180	0	AEA35651	Aea35651 Human NY-
43	89	00	240	6	ADW99402	Adw99402 NY-ESO-1/
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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; long cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; Human cancer antigen NY ESO-1/CAG-3 peptide. vaccine; cytotoxic T lymphocyte; CTL. 98WO-US019609 97US-0061428P (first entry) WO9918206-A2. 21-SEP-1998; 08-OCT-1997; Homo sapiens 15-APR-1999.

(USSH) US DEPT HEALTH & HUMAN SERVICES. Cancer antigen NY ESO1/CAG-3. Wang RF, Rosenberg SA; WPI; 1999-277270/23.

Example 11; Page 50; 88pp; English.

This peptide corresponds to amino acid residues 50-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

Length 14;

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return to a patient
              Query Match
Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9918206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1999.
                                                                                                                                                                                               AAY05978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang RF,
                                                                                                                                                                                                                                                                                                                                                                      vaccine.
                                                                                                                                          RESULT 3
                                                                                                                                                         AAY05978
                                                                                                                                                                                   ઠ
                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAV05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAV05966), portions of them and their carcer vacionses shall be a cancer vacionse that protect against cancer. The invention provides vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; and detection assays; and methods cancer peptide, useful in diagnostic and detection assays; and methods of preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, xidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
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cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                     NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metaetsis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                   ö
                                                                       Length 13;
                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                              Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
                                                                    Query Match 100.0%; Score 68; DB 2; Best Local Similarity 100.0%; Pred. No. 0.017; Matches 13; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                            AAY05986 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; Page 50; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US019609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061428P
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                            1 AARASGPGGGAPR 13
                                                                                                                                                      1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 AA;
                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9918206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1997;
                                                                                                                                                                                                                                                                                  16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1999
                                                                                                                                                                                                                                                        AAY05986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang RF,
                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                               AAY05986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, levisem, cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; netastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
100.0%; Score 68; DB 2;
100.0%; Pred. No. 0.018;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY05978 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0061428P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1999 (first entry)
                                                                                                                                                                           1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                          AARASGPGGGAPR 14
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-277270/23.
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8

8 AARASGPGGGAPR 20

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The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05565), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful; as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; animal; and the cancer peptide or tumour antigen; animals of cancer peptide or tumour antigen; animals of cancer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, ladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NY ESO-1/CAG-3 gene, CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metaetsais; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                      AAY05979 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0061428P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-1999 (fürst entry)
                                                      3 AARASGPGGGAPR 15
1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9918206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                            AAY05979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patient
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                                                                                                                                                                                                                     RESULT 4
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New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.
                                                                    Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonnella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.
AAU85105 standard; peptide; 30 AA.
                                                                                                                                                                       25-MAY-2001; 2001WO-AU000622.
                                                                                                                                                                                         26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                         (AUSU ) UNIV AUSTRALIAN NAT
                                   (first entry)
                                                                                                                                                                                                                           Thomson SA, Ramshaw IA;
                                                    Human NYNSOla segment 4.
                                                                                                                                                                                                                                            WPI; 2002-147575/19.
N-PSDB; ABK36925.
                                                                                                                                   WO200190197-A1.
                                                                                                                  Homo sapiens
                                                                                                                                                     29-NOV-2001.
                                  08-MAY-2002
                 AAU85105;
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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkede in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune response preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cospophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the invention

Example 3; Fig 27; 364pp; English.

Sequence 30 AA;

Gaps ; 0 100.0%; Score 68; DB 5; Length 30; 100.0%; Pred. No. 0.034; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 13; Conservative Query Match

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Query Match 100.0%; Score 68; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 13; Conservative 0; Mismatches 0; Indele

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Gaps

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Gaps

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0; Indels

Pred. No. 0.16; Mismatches

100.08; PE

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13; Conservative

Best Local Similarity

Matches

Cancer associated antigen; NY-ESO-1; regression; progression; onset;

Cancer associated antigen NY-ESO-1.

(first entry)

17-SEP-1998

AAW62584;

cancer; treatment; diagnosis.

Homo sapiens.

AAW62584 standard; protein; 180 AA

AAW62584

/note= "potential myristorylation site" 'note= "potential myristorylation site"

Misc-difference 11

Misc-difference

Location/Qualifiers

Misc-difference Misc-difference note= "potential phosphorylation site"

/note= "potential phosphorylation 'note= "potential phosphorylation

Misc-difference 134

Misc-difference

WO9814464-A1 09-APR-1998.

site"

/note≂ "potential phosphorylation site"

This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate processing by a proteasome; contacting the substrate with a composition including the proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, protozoacide or fungicide activity acting as T-cell activators. In the invention may allow development of a vaccine. The invention contacting the invention may allow development of a vaccine. The invention contacting epitope. The compositions comprising the substrate by proteasome; and substrate by proteasome or in the generation or expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunotherapy. The invention is also useful for activating T-cells against neoplastic cells, and cells infected with contactive protects are in fact. Produced by the contactive for activating T-cells against neoplastic cells, and cells infected with contactive bacterium, protozoan or fungue. CTL epitopes are identified based contactive in fact. Produced by the contactive in the knowledge that such epitopes are, in fact, these epitopes, embodied contactives, can be used in successfully immunise or induce therapeutic contactives, can be used successfully immunise or induce therapeutic contactives. epitope liberation; substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy, neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system; responses against housekeeping proteasome expressing target cells in host. The present sequence is that of a protein which is related to method of the invention. Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope. Epitope liberation-related NY-ESO-1 protein SeqID11. Lei X; Example 2; SEQ ID NO 11; 67pp; English ADK68648 standard; protein; 179 AA. Qiu Z, 07-NOV-2001; 2001US-0336968P. 07-NOV-2002; 2002US-00292413 (first entry) 7 AARASGPGGGAPR 19 Diamond DC, (SIMA/) SIMARD J J L. DIAMOND D C. WPI; 2004-167209/16. N-PSDB; ADK68674 Sequence 179 AA; US2003228634-A1. Homo sapiens. 06-MAY-2004 Simard JJL, 11-DEC-2003 ADK68648; (DIAM/) (QIUZ/) (LEIX/) human CP

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Claim 8; Fig 3; 49pp; English.
                                                                                                    therapeutic regime
                                                                                                       Sequence 180 AA;
                                                                                                          Query Match
100.0%; Score 68; DB 8; Length 179;
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Query Match

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The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NV-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition, for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 68; DB 2; Length 180;
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Knuth A;

Jager E,

old LJ,

Gure A,

Scanlan M,

Drijfhout JW;

Chen Y,

WPI; 1998-286417/25. N-PSDB; AAV38566.

(LUDW-) LUDWIG INST CANCER RES

97WO-US016335.

15-SEP-1997;

96US-00725182

03-OCT-1996;

AAY05965 standard; protein; 180 AA.

RESULT 9 AAY05965 (first entry)

16-AUG-1999

AAY05965;

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The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGB-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an especific for a LAGE-1 TAP comprising contacting an isolated population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of T cells with the cytolytic T cells immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the match and a HLA presenting molecule to selectively enrich an enthod for methods and products from the present invention can be used for the match and a HLA presenting molecule to selectively enrich and a HLA present invention can be used for the products for the present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the pre
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders,
                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methods and products from the present invention can be used for the diagnosis and treatment of LAGB-1 associated disorders, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godelaine D, Boon-Falleur T;
                             0; Indels
  Pred. No. 0.16;
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 57-58; 73pp; English.
                                                                                                                                                                                                                                                            AAW69665 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Smet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US001445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00791495.
                                                                                                                                                                                                                                                                                                                                                                   27-OCT-1998 (first entry)
                                                                                                            50 AARASGPGGGAPR 62
                                                                              1 AARASGPGGGAPR 13
                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-427951/36.
N-PSDB; AAV50348.
     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lucas'S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9832855-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-1998.
                                                                                                                                                                                                                                                                                                                  AAW69665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lethe B,
                             Matches
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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides that protect the recipient from development of cancer. The invention provides: vectors and host cells catransgenic animal; antisense oligonuclectides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods concer peptide, useful in diagnostic and detection assays; and methods concer peptide, useful in diagnostic and detection assays; and methods controlly an without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carvoral cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, and adenocarcinomas such cancer, bladder cancer, liver cancer, and adenocarcinomas such cancer, bladder, pancial and thyroid cancers. Melanoma is treated by inducing cancer, specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                    kidney cancer; pancreatic cancer; liver cancer; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                               NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 68; DB 2; Length 180; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                       tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                          Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US019609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061428P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 1999-277270/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX58599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180 AA;
                                                                                                                                                                                                                                                      bladder cancer;
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                        WO9918206-A2
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RESULT 10

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Gaps

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0; Indels

Mismatches

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Conservative

Local Similarity les 13; Conserv

Matches

Query Match

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100.0%; Score 68; DB 2; Length 180; 100.0%; Pred. No. 0.16;

AAY52430

HLA-

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us-09-529-206e-28.rag

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This sequence represents a human tumour antigen, NY-ESO-1, the CDNA encoding which was isolated from an oesophagus squamous cell cancer CDNA carborary. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and cumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY compensation to the resonant by both MHC (major histocompatibility complex) Cand Class I molecules for presentation to T-cells. Peptides ANY52431-CY5444 bind to Class I HLA-AZ molecules, thereby stimulating compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, or stimulate the proliferation of T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                           note= "Peptide (AAY52434) presented by MHC Class
                                                                             54. .162 -
note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           old LJ;
                                                             "Peptide presented by MHC Class I HLA-B52"
                           "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                         'note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                           note= "Peptide presented by MHC Class I HLA-A3"
159. .167
note= "Peptide presented by MHC Class I HLA-A3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scanlan M, Alexander K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.16;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 30; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                            99WO-US006875.
                                                                                                                                                                                                                                                                                                                                                                                              98US-00165546.
                                                                                                                                                                                                                                                                                                                                                                             98US-00062422
                                                                                                                                                                                                                           .170
                                            .163
                                                                                                             .167
                                                                                                                                                               .166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                notes
                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jager E,
                                                                                                                                                             .58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-038483/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ38380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 180 AA;
                                                                                                                                                                                                                                                                             WO9953938-A1
                                                                                                                                                                                                                                                                                                                                          24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                             17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1998;
                                                                                                                                                                                                                                                                                                           28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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               Peptide
                                            Peptide
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                                                                                                             Peptide
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AAY70862
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145. 153
/note= "Peptide presented by MHC Class I HLA-A24 and HLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Peptide presented by MHC Class I HLA-B7 and HLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-B8
                                                                                                                                          Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytocoxic; helper; etimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; Iymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Peptide presented by MHC Class I HLA-B44"
107. .116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .91
.e= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118. 126
'note= "Peptide presented by MHC Class I HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Peptide presented by MHC Class I HLA-B7, and HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88. 96
/note= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Peptide presented by MHC Class I HLA-A24"
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113. .122
                                                                                                                                                                                                                                                                                                                           .69
e= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                            .53
ce= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                          .68
.e= "Peptide presented by MHC Class I HLA-B7"
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/note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Peptide presented by MHC Class I HLA-B8"
139. .147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Peptide presented by MHC Class I HLA-A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Peptide presented by MHC Class I HLA-A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Peptide presented by MHC Class I HLA-A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                           "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Peptide presented by MHC Class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Peptide presented by
                                                                                                                                                                                                                                                                           Location/Qualifiers
AAY52430 standard; protein; 180 AA.
                                                                                                             Human tumour antigen NY-ESO-1.
                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              88.
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102. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
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                                                               (revised)
                                                                                                                                                                                                                             Homo sapiens,
Unidentified,
                                                           21-OCT-2004
15-FEB-2000
                                                                                                                                                                                                                                                                                          Peptide
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26-JAN-1998;
                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                  old LJ;
                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
AAB69946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma CDNA library. This protein is derived from open reading frame (ORF)—I that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)—recognised Antigen on MELanoma) protein, a tumour-asociated antigen. The tumour-associated antigen. The tumour-associated antigen on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
                                                                                           NY-ESO-1; CAMEL, CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                         Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 68; DB 3; Length 180; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                 ΰ
                                                                                                                                                                                                                                                                                                Klade
                                                                      Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                               Schrier PI, Aarnoudse CA, Heider K,
                                                                                                                                                                                                                                                             (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 62-63; 73pp; English.
AAY70862 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB03154 standard; protein; 180 AA.
                                                                                                                                                                                                             99WO-EP007832
                                                                                                                                                                                                                                      98EP-00119583
                                                                                                                                                                                                                                                                        (UYHO-) UNIV HOSPITAL LEIDEN
                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 AARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                       WPI; 2000-339685/29.
                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD00152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion proteins
                                                                                                                                                              WO200023584-A1.
                                                                                                                                          Homo sapiens.
                                              31-JUL-2000
                                                                                                                                                                                                               15-OCT-1999;
                                                                                                                                                                                                                                      16-OCT-1998;
                                                                                                                                                                                      27-APR-2000
                       AAY70862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB03154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The cDNA encoding this sequence was isolated from a CDNA coll bloady prepared from a specialen of well-tco-moderately differentiated squamous cell cancer of the oesophagea. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma coll innes and in normal ovary and testis tissue, but not in normal collon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The artificen is useful as an immunogen when combined with an adjuvant, in both proteins and post- translationally modified forms, and may be used to precursor and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to oesophageal cancer cells. It can also be used to generate diagnostic or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sahin U, Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                      note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                            'note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                               'note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Potential O-phosphorylation site"
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                                                              'note= "Potential N-myristoylation site"
                                                                                                                                    'note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SLOK ) SLOAN KETTERING INST CANCER RES.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Fig 3; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                             Modified-site
                                                                                               Modified-site
                                                                                                                                                                  Modified-site
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NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLM-DR; cancer; muman leukocyte antigen-determining region; disease progression; disease regression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 68; DB 4; Length 180; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NY-ESO-1 tumour rejection antigen precursor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU01535 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosing testicular tumors.
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                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                             22-JAN-2001; 2001WO-US002126.
                                                                                                                                                                                                                       22-FEB-2000; 2000US-00510635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 13; Conservative
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                                                                                                                                                                                                                                                                                                   Lethe B, Boon-Falleur
                      cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-550091/61.
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH75118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 180 AA;
                                                                                                   WO200162917-A1
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Modified-site
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                                                              Homo sapiens
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                                                                                                                                          30-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining wheher a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                             cytotoxic carcinoma;
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                                                                                                                                                         Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotox
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcino
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 180 AA.
  AAB69946 standard; protein; 180 AA.
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                                                                                                                   Human NY-ESO-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-182822/18.
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                                                                                                                                                                                                                                                                              WO200107917-A1
                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jager E,
                                       AAB69946
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Matches
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Gaps

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Query Match 100.0%; Score 68; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-4) (*)

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Search completed: March 13, 2006, 19:03:59 Job time : 97.8824 secs This Page Blank (uspt⊙)

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GenCore version 5.1.7
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24 ; Search time 15.4471 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-28 68 Perfect score:

1 AARASGPGGGAPR 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query	•			
No.	Score	Match	Length	8	ID	Description
1	44	64.7	82	N	T04476	acclimation protei
7	44	64.7	286	~	S04673	H+-transporting tw
m	44	64.7	379	-	A48082	MAP kinase 3 (EC 2
4	44	64.7	3190	N	T13828	CREB-binding prote
2	43	63.2	185	~	T36874	
9	43	63.2	213	~	S42585	Ψ.
7	43	63.2	222	N	T36115	probable oxidoredu
80	43	63.2	349	~	S55626	hypothetical prote
6	43	63.2	377	~	S28184	Ca2+/calmodulin-de
10	43	63.2		~	JC1451	Ca2+/calmodulin-de
11	43	63.2		~	802165	regulatory protein
12	43	63.2		~	A87431	requlatory protein
13	42	61.8		~	H87399	peptidyl-trna hydr
14	42	61.8		N	G72663	hypothetical prote
15	42	61.8		~	T29031	
16	42	61.8		~	S08341	
17	42	61.8	351	~	S50754	hypothetical prote
18	42	61.8		N	C87425	aldose 1-epimerase
19	42	61.8		~	T52451	endopeptidase Clp
20	42	61.8		N	T36104	conserved hypothet
21	42	61.8		~	G75580	conserved hypothet
22	42	61.8	-	N	T35694	ATP dependent DNA
23	41.5	61.0		~	A29345	steroid hormone re
24	41	60.3	134	N	AB2695	hypothetical prote
25	41	60.3		~	B97477	hypothetical prote
26	41	60.3		7	AB3648	
27	41	60.3	357	~	F82878	XAA-PRO aminopepti
28	41	60.3	371	~	T39312	hypothetical prote
29	41	60.3	389	7	T15102	

tub protein, brain	spidroin 2, dragli	KIAA0641 protein -	DNA-invertase - Sa	hypothetical prote	glycine-rich prote	hypothetical prote	hypothetical prote	Jk-recombination s	androgen receptor	androgen receptor	androgen receptor	heterogeneous nucl	collagen alpha 1 c	tegument protein 6	hypothetical prote
868518	A44112	T00378	JWEBT	T36712	S31415	T17265	A86182	A47214	A34721	B34721	A39248	A44192	A36226	S55659	C72683
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505	627	1207	190	290	291	294	383	575	910	911	919	328	730	3436	103
60.3	60.3	60.3	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.1	58.1	58.1	57.4
41	41	41	40	40	40	40	40	40	40	40	40	39.5	39.5	39.5	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Hordeum vulgare (Darley)
C;Species: Hordeum vulgare (Darley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Plant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRNA stability and localisation of the low temperature responsive barley gene A;Reference number: Z15367; MUID:97299834; PMID:9154983
A;Reference number: Z15367; MUID:97299834; PMID:9154983
A;Recession: T04476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residuse: 1-82 < PMI->
A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:g1418969; P
A;Cross-references: Cv. Igri
C;Genetics:
A;Gene: blt14.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 14;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.7%;
acclimation protein 2 - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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1 AARASGPGGGAP 12

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32 AARGAGAGGVP 43

RESULT 2
S04673
H+transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica C; Becies: Rhodopseudomonas blastica C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004 C; Accession: 804673
R;Tybulewicz, V.L.J.; Falk, G; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription. A; Reference number: S04666; MUID:85058188; PMID:6209404
A; Reference number: S04666; MUID:85058188; PMID:6209404
A; Accession: S04673
A; Accession: Board conceptual translation
A; Molecule type: DNA
A; Residues: 1-286 < TYB>
A; Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C; Superfamily: H(+)-transporting ATP synthase gamma chain
C; Keywords: ATP blosynthesis; hydrolase; membrane-associated complex

Gaps ö 64.7%; Score 44; DB 2; Length 286; 69.2%; Pred. No. 40; i. Mismatches 3; Indels Query Match
Best Local Similarity 69.2
Matches 9; Conservative

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1 AARASGPGGGAPR 13

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Tue Mar 14 10:35:58 2006

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Gaps

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Residues: 1-3190 <AKI>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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A; Reference number: Z17785; MUID: 97263578; PMID: 9109493
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2; Le
Pred. No. 3.2e+02;
1; Mismatches 1;
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A;Molecule type: DNA
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7
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Pred. No. 42;
0; Mismatches
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                                                                                                                                                                                                                                                                                         A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome: transposon Tn163; Superfamily: transposase repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.2%;
72.7%;
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ilarity 77.8%;
Conservative 1
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Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 NGPGGGGPR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 SGPGGGAPR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SCOEDB:SCI51.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 7; Conserv
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                                          A; Accession: T13828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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A; Accession: PQ0270

A; Residues: 14-173, 1',175-379 < COMA

A; Experimental source: call line CEM

R; Gonzalez, F.A.; Raden, D.L; Rigby, M.R.; Davis, R.J.

FEBS Lett. 304, 170-178, 192

A; Attle: Hetrosquencus expression of four MAP kinase isoforms in human tissues.

A; Reference number: S23426; MUD:92316223; PMID:1319925

A; Reference number: S23426; MUD:92316223; PMID:1319925

A; Residues: 25-173 '1', 175-379 < CON>

A; References: UNIPARC:UPI000016A2B4; EMBL:211696; NID:923882; PIDN:CAA77754.1; PIL

C; Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).

C; Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).

C; Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).

C; Complex: monomer: GB: 135679; OMIM:601795

A; Gone: GB: PRKM3; ERR

A; Cross-references: GB: 135679; OMIM:601795

A; Gone: Complex: monomer: Gpter-16qter

C; Complex: monomer: Gpter-16qter

C; Complex: monomer: Spter-16qter

C; Complex: monomer: This enzyme related transforming protein; protein kinase enscade

C; Superfamily: kinase-related transforming protein; protein kinase accade

C; Superfamily: kinase-related transforming protein; protein kinase ATP-binding protein; protein kinase ATP-binding protein; E; 40-56/Region: protein kinase ATP-binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted

F; 202/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted

F; 204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase)
                                                                                                                                                                                                                         Note: authors translated by CCL 2.7.1.9.7

Note: Allernate names: extracellular signal-regulated kinase 1 (ERKI); mitogen-activated procession: Structure names: extracellular signal-regulated kinase 1 (ERKI); mitogen-activated by Contains: protein kinase (EC 2.7.1.37)

C; Species: Homo sapiens (man)
C; Date: 04-Sep-1998 #sequence revision 04-Sep-1998 #text_change 09-Jul-2004
C; Accession: A48082; PQ0270; $23428; S15519; S21579
R; Chartest, D.L.; Mordret, G.; Harder, K.W.; Jürik, F.; Pelech, S.L.
Nol. Cell. Biol. 13, 4679-4690, 1993
A; Title: Molecular cloning, expression, and characterization of the human mitogen-activa h; Recence number: A48082; MUID:99330262; PMID:7687743
A; Maccession: A48082
A; Molecula trype: mRNA
A; Residues: 1-379 cHA>
A; Rosidues: 1-379 cH
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Askimaru, H.; Ohen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Gd
Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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CREB-binding protein homolog - fruit fly (Drogophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 64.7%; Score 44; DB 1; Length 379; Best Local Similarity 69.2%; Pred. No. 51; Matches 9; Conservative 0; Mismatches 4; Indels
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54 ASLASGOGAGAPR
                                                                                                                                                                                                        MAP kinase 3 (EC 2.7.1.-)
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A;Molecule type: DNA
A;Residues: 1-213 <ULR>
A;Cross-references: UNIPROT:Q52760; UNIPARC:UPI0000AE947; EMBL:L14931; NID:G349099; PID
A;Experimental source: strain E163N; class II transposon Th163
C;Genetics:
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q98229; UNIPARC:UPI0000DB31A; EMBL:AL109848; PIDN:CAB52835 A;Experimental source: strain A3(2) C;Ganetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: resolvase
C;Species: Rhizobium leguminosarum
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 842885
R;Ulrich, A.; Puehler, A.
Roll Gene. 242, 505-516, 1994
A;Title: The new class II transposon Tn163 is plasmid-borne in two unrelated Rhizobium A;Reference number: 842584; MUID:94166763; PMID:8121409
hypothetical protein SCI51.11c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Dacession: 136874
C;Accession: 136874
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: DNA binding; DNA integration; DNA recombination F;11/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-invertage - Rhizobium leguminosarum transposon Tn163
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A;Molecule type: mRNA

A;Rebidues: 74-377 -CDEN-

A;Rebidues: 74-377 -CDEN-

A;Cross-references: UNIPARC:UPI0000023599; GB:S59517

B;Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.

B;Ccrews, C.M.; Alessandrini, A.A.; Erikson, R.L.

B;Cc. Natl. A;Cad. Sci. U.S.A. 88 , 8845-8849, 1991

A;Title: Mouse Brk-1 gene product is a serine-(threonine protein kinase that has the pot

A;Reference number: A41371; MUID:92020947; PMID:1717989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UP10000170C57; GB:SS8470; NID:9236372; PIDN:AAB19973.1; PID C;Superfamily: kinase-related transforming protein; protein kinase homology C;Kywords: ATP; calmodulin binding; phosphotransferase; protein kinase F;38-328/Domain: protein kinase homology <KIN: F;46-54/Region: protein kinase ATP-binding motif
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A;Residues: 1-380 cMAR.
A;Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X65198; NID:g56626; PID.
A;Experimental source: brain
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A.Title: An insulin-stimulated protein kinase similar to yeast kinases involved in cell A; Reference number: A35061
A.Molecule type: mRNA
A.Molecule type: mUNIPARC:UPI0000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID
A.Molecule type: mRNA
A.Molecule type: mUNIPARC:UPI000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID
A.Molecule type: mRNA
A.Molecule type: mVNIPARC:UPI000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID
A.Molecule type: mVNIPARC:UPI000145072; PIDN:AAA41123.1; PIDN:AAA4112
A;Cross-references: UNIPROT:063844; UNIPARC:UPI000017558C; EMBL:214249
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse A;Reference number: A40466; MUID:91369479; PMID:1716439
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A; Residues: 43-64;167-178, XX', 180-183, XX', 185 < BO2>

A; Residues: 43-64;167-178ARC: UPI000017558F; UNIPARC: UPI0000175590

B; De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.

NA Cell Biol. 10, 505-514, 1991

A; Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse

A; Reference number: A40466; MUID: 91369479; PMID: 1716439
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NyAlternate names: ERK1-MAP kinase; extracellular signal-regulated kinase
Cispecies: Rattus norvegiuse (Norway rat)
Cipate: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
Cipate: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
Cipate: 30-Sep-1993 #scauce revision 30-Sep-1993 #text_change 09-Jul-2004
Cipate: 30-Sep-1993 #scauce of a rat cDNA encoding the ERK1-MAP kinase.
A;ritle: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
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69.2%; Pred. No. 69;
iive 0; Mismatches
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A;Molecule type: mRNA
A;Residues: 14-94,'R',96-380 <DEM>
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ses 9; Conserv
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A; Residues: 7-16 < CRE>
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Submitted to the EMBL Data Library, April 1999

Submitted to the EMBL Data Library, April 1999

Streference number: Z21597

A; Reference number: Z21597

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-222 < MUR>
A; Residues: 1-222 < MUR>
A; Residues: 1-222 < MUR>
A; Experimental source: strain A3(2)

A; Experimental source: strain A3(2)

A; Genetics: A; Genetics: C; Superimental source: Strain A3(2)

A; Superimental source: Strain A3(2)
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C;Species: Mus muscudus (house mouse)
C;Date: 22-Nov-1993 Haequence revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S28184; B40466; Ā41371
B;Tanner, B.; Mueckler, M.
B;Accession: S1, Mueckler, M.
A;Title: Molecular cloning of a mouse extracellular signal regulated kinase (erk-1). A;Reference number: S28184; MUID:93144347; PMID:84957
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C;Species: equine herpesvirus 2

C;Species: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S55626

B.Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A.Title: The DNA sequence of equine herpesvirus 2.

A.Reference number: S55594; MUID:95302501; PMID:7783207

A.Accession: S55626

A.Status: preliminary; nucleic acid sequence not shown; translation not show
                                                                                                                                                                                                                                                                                                                                                        probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
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65;
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Pred. No. 44;
1; Mismatches
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                         1 AARASGPGGGAP 12
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Best Local Similarity
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Matches 9; Conserv
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R; Murphy, L.; Harrie
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RESULT 11

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peptidy1-tRNA hydrolase [imported] - Caulobacter crescentus
C; Bate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Bate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Baccession: H8739
C; Rocession: H8739
B.; Remolaeva, W.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary
Modecule type: DNA
A,Residues: 1-143 «STD»
A,Cross-references: UNIPROT:Q9A8Y3; UNIPARC:UPI00000C72F1; GB:AE005673; NID:g13422540; 1
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72663
C;Accession: G72663
R;Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Takal awa, H; Takamiya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; k DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72663
A;Status: preliminary
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0734
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submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F53G12.
A;Reference number: Z20555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F53G12.7 - Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-327 <WUX>
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Pred. No. 56;
0; Mismatches
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Pred. No.
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88.9%;
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity
8; Conserv?
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A; Residues: 1-201 < KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CC1214
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldhlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Aconglete Genome Sequence of Caulobacter crescentus.
A;Reference number: A8743;
A;Reference number: A8743;
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-954 <STO>
A;Residues: 1-954 <STO>
A;Genetics:
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R; Kaplan, J. B.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
R; Kaplan, J. B.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 206, 71-83, 1989
A; Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A; Reference number: S02164; MUID:89178645; PMID:2648000
A; Accession: S02165
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-679 < KAP>
A; Residues: 1-679 < KAP>
A; Cross-references: UNIPROT:P15345; UNIPARC:UPI000017A8F7
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Keywords: transcription regulation
   A;Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:g515498; PIDN:AAA2d C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords. ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin F;41-31/Domain: protein kinase homology «Kin. F;41-31/Domain: protein kinase ATP-binding motif
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C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
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Pred. No. 1.2e+02;
0; Mismatches 4; Indels
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Pred. No. 70;
0; Mismatches
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66.7%;
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9; Conservative
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Best Local Similarity 66.7
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.

MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
"A testicular antiogen aberrantly expressed in human cancers detected
by autologous antibody screening.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 68; DB 2; Length 142; 100.0%; Pred. No. 0.057; ive 0; Mismatches 0; Indels
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Last annotation update)
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15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                  Q81VQ3_HUMAN
Q4NN12_9DELT
Q9GRA8_GRYBI
05SQT4_HUMAN
0688D5_GRYSA
051415_PSEAB
Q4T32_TETNG
G55MM1_CRYNB
Q4P99_USTWA
Q4PH9_USTWA
Q4PH9_USTWA
Q4PH9_USTWA
Q4PH9_USTWA
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Homo sapiens (Human).
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01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein LAGE-2
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Q9NY13;
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es 13; Conservative
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CTG1B HUMAN
ID CTG1B HUMAN
AC P78358;
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  Query Match
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                                                                                                                                                March 13, 2006, 18:53:23 ; Search time 94.3647 Seconds (without alignments) 97.196 Million cell updates/sec
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Gaps

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NCBI_TaxID=9606;
Nelson D.L.;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                       Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T., 1.
Hadel, a new gene with tumor specificity.";
"ILAGE-1, a new gene with tumor specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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--- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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Pred. No. 0.071;
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Gly-rich.
; B122C5C2C8BE1569 CRC64;
  Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997)
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Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
Homo sapiens (Human).
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EMBL; AF038567; AAD05202.1; -; mRNA.
HGNC; HGNC:2491; CTAGIB.
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Q7LBY4 HUMAN PRELIMINARY;
Q7LBY4;
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Best Local Similarity 100.
Matches 13; Conservative
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                                            NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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                                                              TISSUE=Melanoma;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=98289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen E., Boon T.;
"LAGB-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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GLN-6; GLN-89 AND ARG-138.
"Multiple pathogenic and benign genomic rearrangements occur at
kb duplication involving the NEMO and LAGE2 genes.";
Hum. Mol. Genet. 10:2557-2567(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set
line- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAG2 HUMAN STANDARD; PRT; 210 AA.
O75638; O75637; Q9BU80; Q9U389; Q9Y479;
30-MAY-2000 (Rel. 39, Careated)
30-MAY-2005 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
EMBL; AZ275315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SEQUENCE 180 AA; 17992 MW; B122C5CZC8BE1569 CRC64;
                                                                                                                                                                                                           Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                             Figure M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                            Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 68; DB 2; 100.0%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=CTAG2; Synonyms=ESO2, LAGE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                          NUCLEOTIDE SEQUENCE
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us-09-529-206e-28.rup

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TISSUE=Placenta;

X MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

A Altschul S.F., Joordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Rabla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Radiques S., Sanchez A.,

X Hallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hallon D.K., Muzny D.M., Garcia A.M., Rodrigues S., Sanchez A.,

X Hallon B., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,

X Hallesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

X Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \begin{array}{lll} \text{Pol}_{Y^{-}P\Gamma O}, \\ \text{MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV} \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-18), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms=2;
Name=LAGE-1B; Synonyms=LAGE-1L;
IsoId=075638-1L; Sequence=Displayed;
Name=LAGE-1A; Synonyms=LAGE-1S;
IsoId=075638-2; Sequence=VSP 004301;
TISSUE SPECIFICITY: Testis and very low level in placenta and in some uterus samples. Observed in 25-50% of tumor samples of melanomas; Pon-small-cell lung carcinomas; bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing; Antigen; Polymorphism; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 1; Length 210;
Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRR (in isoform LAGE-1A).
/FTId=VSP_004301.
R -> Q.
/FTId=VAR_007855.
                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E -> Q.
/FTId=VAR_007856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AJ223093; CAA11117.1; -; Genomic_DNA.
EMBL, AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL, AJ223040; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
EMBL, AJ012834; CAA10194.1; -; mRNA.
EMBL, AJ012835; CAA10196.1; -; mRNA.
EMBL, BJ012835; CAA10196.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG0000126890; Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.2%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         head and neck cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.3
Matches 12; Conservative
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188
210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
NCBI_TaxID=28450;
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25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymeraes III, delta subunit (EC 2.7.7.7).
Name=holA; OrderedLocusNames=BMA2451;
Burkholderiaeeaei Burkholderiaeeae; Burkholderiaeeae; Burkholderiae
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PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
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Pred. No. 13;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                        362 AA
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                           Created)
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1 Similarity 83.3%;
10; Conservative
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                                                                                                                                                                                                                                                                    QG3QT8 BURPS PRELIMINARY;
Q63QT8;
1 AARASGPGGGAPR 13
                                                                          50 AARASGPRGGAPR 62
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Q62H22;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K96243;
                                                                                                                                                                                                                                       SURPS
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DT 255

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Gaps

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1; Indels

0; Mismatches

us-09-529-206e-28.rup

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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
    Hypothetical protein OSJNBa0063J18.9.
                  Name=OSJNBa0063J18.9;
                                                                                NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.,
"Structural flexibility in the Burkholderia mallei genome.";
Ernctural flexibility in the Burkholderia mallei genome.";
EMBL, CP000010; AAU49707.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daniels R.J., Peden J.F., Iloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339; Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
                                                                                                                           GO; 60:0003887; F:DNA-directed DNA polymerase activity; IEA. GO; GO:00056740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0006260; P:DNA replication; IEA. InterPro; IPR010372; DNA pol3 delta. InterPro; IPR05790; DNA pol1II delta. PF06144; DNA pol3 delta. TIGRPAMS; TIGR01128; holA; 1.
                                                                                                                                                                                                                                                             Score 54; DB 2; Length 362;
Pred. No. 13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.5%; Score 52; DB 2; Length 321; 76.9%; Pred. No. 22; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                       Complete proteome, Nucleotidyltransferase, Transferase. SEQUENCE 362 AA, 38726 MW, D5FP3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Q96827 HUMAN PRELIMINARY; PRT; 321 AA. 096827.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Name-gene X; Human gene X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE006463; AAK61225.1; -; Genomic DNA.
Ensembl; ENSG00000167933; Homo sapiens.
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                                                                                                                                                                                                                                                                 79.4%;
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QEAV33;
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Best Local Similarity 76.9
Matches 10; Conservative
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Matches 10; Conserv
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                                                                                                                      TIGR; BMA2451;
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25-OCT-2004
25-OCT-2004
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ID QGAV33 OR
AC QGAV33;
DT 25-0CT-21
DT 25-0CT-21
                                                                                                                                                                                                                                                                Query Match
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ALLSCHEREZEGES;

RA PEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Strausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hisieh F.,

By Listchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RACHERO S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards J., Hellon B.K., Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

R. Gennerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodriguez A.C., Grimwood J.S., Schmutz J., Mysra R.M.,

R. Rodriguez A.C., Grimwiski M.I., Skalska U., Smallus D.E.,

R. And Mala A. Jones M. J. Marra M.A.;

R. Rodriguez A.D., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodriguez A.D., Schein J.E., Jones E.D., Dickson M.C.,

R. R. Rodriguez A.D., Schein J.E., Jones B.J.M., Marra M.A.;

R. Rodriguez A.D., Schein J.E., Jones B.J.M., Marra M.A.;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBAOOG3J18 genomic sequence.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2; Pred. No. 35; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AC107206; AAT77052.1; -; Genomic_DNA.Gramene; Q6AV33; -.
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76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 76.9
nes 10; Conservative
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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A Straubberg R.L., Feinged E.A., Grouse L.H., Derge J.G., Nauner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachul R.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bran S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bran S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abran S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abran S.S., McKernan R.J., Malke J.A., Gunber R.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Andlan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abranch B. Ketreman M., Wyers R.M., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.M., Marra M.A., Schein J.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%; Score 50; DB 2; Length 896; 81.8%; Pred. No. 1.1e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Director MGC Project;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013422; AAH13426.1; -; mRNA.
SEQUENCE 896 AA; 94247 MW; ODE6869BCFD4C471 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLEKHG2 protein (Fragment).
Name=PLEKHG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dehalogenans 2CP-C.";
Submitted (JUN-2005) to the BMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=AdehDRAFT 2813;
Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                     Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 895;
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76.9%; Pred. No. 1.18+02;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                       Indels
                NUCLEOTIDE SEQUENCE.
TISSUE=Pancreas;
Director MGC Project;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015174; AM115174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
1, AAHD01000013; EAL79351.1; -; Genomic DNA.
JENCE 895 RA; 93871 MW; 0AE25BBBF17ZBDB0 CRC64;
                                                                                                                                                  NON TER 1 1
SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                  Score 50; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Name=PLEKHGZ protein.

Name=PLEKHGZ;

Homo sapiens (Human).
                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797 ARRARGAGGAPR 809
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Q96D18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4NUK4 9DELT PRELIMINARY;
Q4NUK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AARASGPGGGAPR 13
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          99 ARROGPGGGAP 109
                                                                                                                                                                                                                                                                                                                                         2 ARASGPGGGAP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=290397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005
13-SEP-2005
                                                                                                                                                                                                                                                                                       .
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Q96D18_HUN
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Name=ADCYAP1;
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SEQUENCE
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PubMed=14702039; DOI=10.1038/ng1285;

PubMed=14702039; DOI=10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Tanaka T.,

Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

Sugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa B.,

Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,

Pujimori K., Tanai H., Kimta M., Watanabe M., Hiraoka S., Chiba Y.,

Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T.,

M. Kusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O.,

Nomura Y., Matsunawa H., Ichihara R., Takeuchi K., Arita M.,

Imose N., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

A Ishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 2; Length 1253;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                               Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 PH domain.
EMBL, BCOSSSS, AMTHSSS.1; -; mRNA.
INTERPRO; IPRO01849; PH.
InterPro; IPRO01849; PH.
InterPro; IPRO0189; Ph.OGBF.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
SMART; SM00135; RhoGEF; 1.
SWART; SM00135; RhoGEF; 1.
PROSITE; PSS0001; DH_2; 1.
PROSITE; PSS0001; DH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                        1253 AA; 134404 MW; 534EB31283E535C5 CRC64;
                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLJ00018 protein (Fragment).
Name=PLEKHG2; Synonyms=FLJ00018;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                   73.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H7P9 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1158 ARRQCPGGAP 1168
                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ARASGPGGGAP 12
                                                                                                                                                                       TISSUE=Pancreas;
Director MGC Project;
                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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PACA_CHICK STANDARD; PRT; 175 AA.
P41534; O55WW0;
01-NOV-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Glucagon-family neuropeptides precursor [Contains: Growth hormone-releasing factor 1-66 (GRF) (Growth hormone-releasing factor 1-66 (GRF) (Growth hormone-releasing hormone) (GHRH); Pituitary adenylate cyclase activating polypeptide-27 (PACAP-27) (PACAP-27)
(PACAP-38) (PACAP-38)
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NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].

MEDLINE=97174314; PubMed-9022048;

MCRORY J.E., Parker R.L., Sherwood N.M.;

MCRORY J.E., Parker R.L., Sherwood N.M.;

"Expression and alternative processing of a chicken gene encoding both growth hormone—releasing hormone and pituitary adenylate cyclase—
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Pujiwara T., Pujiwara T., Pujiwara T., Pujiwara T., Amaigami A., Pujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matemura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Makagawa K., Okumura K., Nagase T., Nomura Y., Okara O., Kablashi Y., Nakagawa K., Okumura K., Nakagara Y., Ohara O., Isogai T., Sugano S., Nakamura Y., Ohara O., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 131-168.

Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;

Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;

Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;

Regul, Pept. 37:326-326(1992).

-!- FUNCTION: Primary role of GRP is to release GH from the pituitary.

-!- FUNCTION: PRAMP plays pivotal roles as a neurotransmitter and/or a neuromodulator.

-!- SUBCELLUIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1430 AA; 152528 MW; E4DF0BFDACCB6A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl, ENSG00000090924; Homo mapiens.
HGNC; HGNC:29515; PLEKHG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Genet. 36:40-45(2004).
-!- SIMILARITY: Contains 1 PH domain.
EMBL; AK024429; BAB15719.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001849; PH.
InterPro; IPR001919; RhoGBF.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGBF; 1.
SWART; SM00235; RhoGBF; 1.
SWART; SM00325; RhoGBF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS500010; PH DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activating polypeptide.";
DNA Cell Biol. 16:95-102(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1335 ARROGPGGGAP 1345
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q64096; 1KZ7
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Gaps
  "Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism.", Nucleic Acids Res. 32:4937-4944(2004).
                                                                   EMBL; AP006040; BAD40403.1; '; Genomic DNA.
GO; GO:0004665; F.prephenate dehydrogenase (NADP+) activity; IEA.
GO; GO:0006571; P:tyrosine biosynthesis; IEA.
InterPro; IPR003099; Prephen_dehydrog.
Pfam; PF02153; PDH; 1.
Complete protecome.
SEQUENCE 322 AA; 32843 MW; 09A06ACOAFA734EC CRC64;
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                                                                                                                                                                                                                                                                  Score 49; DB 2; Length 322;
Pred. No. 58;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 13, 2006, 19:14:27 Job time: 94.3647 secs
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                 1 AARASGPGGGA 11
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                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000532; Glucagon.
Pfam; PR010123; Hormone 2; 2.
PRINTS; PR00275; GLUCAGON.
Alternative splicing; Amidation; Cleavage on pair of basic residues; Direct protein sequencing; Glucagon family; Hormone; Signal.
23 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pituitary adenylate cyclase activating polypeptide-38. Pituitary adenylate cyclase activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group).
RHADGIFSKAYRKLLGQLSARNYLHSLMAKRVG ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth hormone-releasing factor 1-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leucine amide (G-158 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lysine amide (G-169 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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PubMed=15383646; DOI=10.1093/nar/gkh830;
Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Morimura K., Ikeda H., Hattori M., Beppu T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in isoform GRF 33-46).
/FT1d=vSP 001759.
Missing (In isoform GRP 1-43)
/FT1d=vSP 001760.
0DB54995F0AA9DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 1; Length 175;
Pred. No. 33;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Prephenate dehydrogenase.
                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                 IsoId=P41534-3; Sequence=VSP_001759;
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide-27
                                                                                                                    IsoId=P41534-2; Sequence=VSP_001760;
                                            Name=GRF 1-46;
IsoId=P41534-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; U71184; AAB51200.1; -; mRNA.
EMBL; U71184; AAB51201.1; -; mRNA.
EMBL; U71185; AAB51202.1; -; mRNA.
EMBL; U67275; AAC64494.1; -; Genomic_DNA.
HSSP; P18509; IGEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Symbiobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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ALTERNATIVE PRODUCTS
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067920 SYM
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Sequence:

Run on:

Searched:

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No.

Result

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23, Appl
28380, A
8, Appli
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14, Appl
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Sequence 4, Appli
Sequence 59895, A
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US-09-252-991A-27111

US-09-902-540-12383

US-09-902-540-16943

US-09-861-012A-23

US-09-861-012A-23

US-09-861-09-23

US-09-861-09-23

US-09-861-09-23

US-09-252-991A-28380

US-09-252-91A-28380

US-09-252-91A-28380

US-09-252-91A-28380

US-09-252-91A-28

US-09-253-90-25

US-09-411-628-14

US-09-538-092-1021

US-09-642-749-25

US-08-417-19-39

US-08-417-19-39

US-08-938-291A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TEADABLE FORM:

COMPUTER TEADABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/791,495

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Leth, Bernard
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                    US-09-270-767-59895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Ameterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 13; Conservative
  MOLECULE TYPE: protein US-08-791-495-9
  STREET: 600 A
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Sequence 8, Appli
Sequence 25, Appli
Sequence 15, Appli
Sequence 30, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 17, Appli
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Sequence 117, Appli
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Sequence 317, Appli
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Sequence 31759, A
Sequence 20577, A
Sequence 24923, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25611, A
Sequence 29442, A
Sequence 3295, Ap
                                                                                                                              March 13, 2006, 19:14:49; Search time 24.1647 Seconds (without alignments) 44.477 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
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US-09-371-263B-8
US-09-371-263B-8
US-09-392-714-25
US-09-165-546D-15
US-09-341-829A-9
US-09-341-829A-9
US-09-341-829A-9
US-09-341-829A-9
US-09-341-829A-7
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US-09-252-991A-32326
US-09-252-991A-20577
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                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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                                                                         APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander; Knuth; Drijfbout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATEL: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Aso-tseng; Scanlan, Matthew;
ATTLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: 1EM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:

NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 8:
SEQUENCE CHARACTERISTICS:
Sequence 8, Application US/08937263B
Patent No. 6274145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09751798
Patent No. 6525177
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AARASGPGGGAPR 13
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100.0%; Pred. No. 0.068;
tive 0; Mismatches 0; Indels
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US-09-392-714-25

Sequence 25, Application US/09392714A

Patent No. 6666147

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Ali O.
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: Therefor
FILE REFREENCE: L0461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 25.
CUCUMALY.

ZIP.

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                                                                                                                                                                                                        OPERATING SYSTEM: FC.C.
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: OCCODER 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HAINSON, NO. 6528177man D.
REGISTRATION NUMBER: 30,946
REPRENCE/DOCKET NUMBER: LUD 5466.:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENNATH: 180
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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US-09-392-714-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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    <151> 1998-01-27
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Chen, Yao-Tseng
ITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849, 602
CURRENT FILING DATE: 2001-05-04
NUMBER: OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 68; DB 2;
100.0%; Pred. No. 0.068;
iive 0; Mismatches 0
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GENERAL INFORMATION:

APPLICANT: Leth , Bernard

APPLICANT: Lucas, Sophie

APPLICANT: De Smet, Charles

APPLICANT: Godelaine, Daniele

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                           Mismatches
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7, Application US/08791495
; Patent No. 5811519
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600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                    1 AARASGPGGGAPR 13
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                                                                                                                                                                                                                                                         Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-341-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserval
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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ZIP: 02210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                TYPE: PRT
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                                                                                                         APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Sure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811) TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 68; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 0.068; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION PARTS:

MEDIUTER: IBM
COMPUTER: IBM
COBERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Good-Falleur, Thierry
IITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422

FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997

APPLICATION NUMBER: US 08/725,182

FILING DATE: OCCODER 3, 1996
                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 6723832man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
                                           Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 318-3000
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Patent No. 6794131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 180 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                     US-09-165-546D-15
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                   COUNTRY:
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APPLICANT: Lucas, Sophie
APPLICANT: Ducas, Sophie
APPLICANT: De Smet, Carries
APPLICANT: Godelaine, Daniele
CURRENT GODELICATION NUMBER: US/09/341,829A
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT APPLICATION NUMBER: PS/08/01445
PRIOR APPLICATION NUMBER: PCT/US/98/01445
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NO 7.0
                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 1; Length 180;
Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

88.2%; Score 60; DB 2; Length 180;
Best Local Similarity 92.3%; Pred. No. 0.75;
Matches 12; Conservative 0; Mismatches 1; Indels
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Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
CORRESPONDENCE ADDRESS:
PPLICALL...
PPLILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
TELECHONTINICATION INFORMATION:
TELEPRAX: 617-720-3500
TELEPRAX: 617-720-341
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
"VIR' amino acids
"VIR' amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: 1:4
                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.2%;
Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-791-495-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-341-829A-7
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US-08-791-495-5
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Pred. No. 0.86;
0; Mismatches 1; Indels
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                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 210
TYPE: PRT
                                                                                                                                                                                                                                                                                L0461/7005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-341-829A-5; Sequence 5, Application US/09341829A; Patent No. 6794131
                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELEPOMONICATION INFORMATION:
TELEPOMONE: 617-720-3500
TELEPHONE: 617-720-3500
 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%;
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 210 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AARASGPRGGAPR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-341-829A-5
                                                 USA
STREET: 600 A
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Gaps
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                                                                           Length 143;
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                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08789329C
Patent No. 6165755
GENERAL INFORMATION:
TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSER: Klarquist Sparkman Campbell Leigh & ADDRESSER: Klarquist Sparkman Campbell Leigh & ADDRESSE: Whinston, LLP STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: 121 S.W. Salmon Street STREET: 121 S.W. Salmon Street STREET: Suite 1600 CITY: Portland STATE: Oregon COUNTRY: United States of America ZITY: Portland STATE: Oregon COUNTRY: United States of America ZIP: 97204-2988 COMPUTER READABLE FORM: Windows NT SOFTWARE: WordPerfect 7.0 & ASCII CURRENT APPLICATION DATA: US/08/789,329C FILING DATE: 01/23/97 CLASSIFICATION NUMBER: US/08/789,329C FILING DATE: CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PILING DATE: CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PILING DATE:
                                                                           Score 49; DB 2;
Pred. No. 16;
0; Mismatches
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Sequence 3, Application US/08789329C

Patent No. 616575

GENERAL INFORMATION:

APPLICANT: SHERWOOD ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Earp, David J.
REGIGTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 2847
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                              72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 172 aa
                                                                                                                                                                               1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                  54 ALRAGAPGGGGPR 66
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                                                                           Query Match 72.1
Best Local Similarity 69.2
Matches 9; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
          , 10F0L021:
US-08-789-329C-10
                                                                                                                                                                                                                                                                                                                                         US-08-789-329C-7
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        Sequence 17249, Application US/09252991A

Sequence 17249, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17249

LENGTH: 160
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US-08-789-329C-10
Sequence 10, Application US/08789329C
i Patent No. 6165755
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
TITLE OF INVENTION: POR IMPROVED POULTRY PRODUCTION
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Whinston, LLP
STREET: 121 SW. Salmon Street
STREET: One World Trade Center
STREET: Oregon
CITY: Portland
STREET: Oregon
COUNTRY: United States of America
STREET: Oregon
CONVIRY: United States of America
STREET: Oregon
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: NordPerfect 7.0 & ASCII
COMPUTER: WordPerfect 7.0 & ASCII
CURSETICATION NUMBER: US/08/789,329C
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATE:
BRING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.5%; Score 50; DB 2; Length 160; 69.2%; Pred. No. 13;
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REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 2847-46468/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AGRRAGEGGSAPR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.5
Best Local Similarity 69.2
Matches 9; Conservative
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TYPE: amino acid
STRANDEDNESS: single
US-09-252-991A-17249
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TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
TITLE OF INVENTION: CRI IMPROVED POULTRY PRODUCTION
CORRESPONDENCE: 20
CORRESSEE: Winston. Lib.
ADDRESSEE: Winston. Lib.
ADDRESSEE: Winston. Lib.
STREET: 0.0 World Tada Center
STREET: 0.12 s.w. Salmon Street
STREET: 0.13 s.w. Salmon
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Search completed: March 13, 2006, 19:18:51 Job time : 24:1647 secs

| || ||| || 54 ALRAGAPGGGGPR 66

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US-10-42

Sequence 202, Application US/10482029

; Sequence 202, Application US/10482029

; Publication No. US20050037445A1

; GENERAL INFORMATION:

; APPLICANT: ODIN medical A/S

; TITLE OF INVENTION: Oncology drug innovation

; TILE REFERENCE: P 573 PC00

; CURRENT APPLICATION NUMBER: US/10/482,029

; CURRENT PILING DATE: 2003-12-29

; NUMBER OF SEQ ID NOS: 437

; SEQ ID NO 202

; LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-10-482-029-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
 TYPE: PRT
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Sequence 202, App
Sequence 8, Appli
Sequence 30, Appl
Sequence 8, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             March 13, 2006, 19:51:56; Search time 78.6118 Seconds (without alignments) 69.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 386, Sequence 832, Sequence 139, Sequence 11, A
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Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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Sequence 7
Sequence 1
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
cgn2_6/prodata/1/pubpaa/USO9_PUBCOMB.pep:*
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cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-296-734-1404
US-10-482-029-202
US-09-849-602-30
US-09-849-602-30
US-10-021-182-8
US-10-207-655-71
US-10-207-655-71
US-10-206-734-832
US-10-296-734-832
US-10-296-734-832
US-10-296-734-832
US-10-296-734-832
US-10-296-734-832
US-10-296-734-832
US-10-296-734-832
US-10-296-734-832
US-10-657-022-74
US-10-657-022-74
US-10-657-023-71
US-10-877-373-9
US-11-667-054-74
US-11-667-054-74
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA_Main:*
                                                                                                                                                                                                                    1867569 segs, 417829326 residues
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                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                        1 AARASGPGGGAPR 13
                                                                                                                              US-09-529-206E-28
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0
                                                                                                                               Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                    Searched:
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                                                                                Run on:
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No.
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Appli
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Sequence 496, App
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                                       Sequence Sequence
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Sequence
Sequence
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Sequence
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Sequence
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; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SEQ ID NO 1404
; LENGTH: 30
; TENDER OF SECOND NOS: 1507
; SEQ ID NO 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 100.0%; Score 68; DB 4; Length 30; Similarity 100.0%; Pred. No. 0.076; 13; Conservative 0; Mismatches 0; Indels
US-10-296-734-1436
US-10-298-734-1436
US-10-146-473-69
US-10-146-473-69
US-10-146-473-69
US-10-146-473-69
US-10-146-473-69
US-10-657-022-75
US-10-657-022-75
US-11-067-159-75
US-10-117-937-76
US-10-657-022-76
US-10-657-022-76
US-10-657-022-76
US-10-657-022-76
US-10-657-022-76
US-10-657-022-76
US-11-067-064-76
US-11-067-064-76
US-11-067-064-76
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Stockert, Elisabeth
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                                                                                                                                                                                                                                                              Sequence B, Application US/09751798
| Patent No. US200201010321A1
| GENERAL INFORMATION:
| APPLICANT: Stockert, Elisabeth; Jager, Elke;
| APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
| APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
| APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
| APPLICANT: Knuth, Alexander; Old, Lloyd J.
| TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 cancer: TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1, and HLA TITLE OF INVENTION: Binding Peptides Derived Therefrom NUMBER OF SEQUENCES: 8
| CORRESPONDENCE ADDRESS: ADDRESSE: Fulbright & Jaworski, L.L.P.
| STRRET: 666 Fifth Avenue CITY: New York City STRATE: New York City STRATE: New York City STRATE: New York City
                                                  ö
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Query Match 100.0%; Score 68; DB 5; Length 179; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 13; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.37;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERSFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEG ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                   1 AARASGPGGGAPR 13
                                                                                                                                              50 AARASGPGGGAPR 62
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-751-798-8
                                                                                                                                                                                                                     RESULT 3
US-09-751-798-8
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RESULT 4
US-09-849-602-30
| Sequence 30, Application US/09849602
| Publication No. US20030165834A1
| GENERAL INFORMATION
| APPLICANT: Scanlan, Matchew J.
| APPLICANT: Old, Lloyd J.

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Gaps
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Chen, Yao-tseng; Scanlan, Mathew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
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                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 68; DB 3; Length 180; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 13; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Valbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, No. US20020164665Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: LO461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 1BM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: «Unknown-
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AARASGPGGGAPR 62
                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-849-602-30
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Gaps
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100.0%; Pred. No. 0.37;
Live 0; Mismatches 0; Indels
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                      | GENERAL INFORMATION: |
| APPLICANT: Simard, John J. L. |
| APPLICANT: Simard, John J. L. |
| APPLICANT: Simard, John J. L. |
| APPLICANT: Diamond, David C. |
| TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN |
| TITLE OF INVENTION: PRESENTING CELLS |
| FILE REFERENCE: CTLINM.12CPLC |
| CURRENT APPLICATION NUMBER: US/10/026,066 |
| CURRENT APPLICATION NUMBER: 09/561,074 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR PLICATION NUMBER: 09/561,571 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2001-04-27 |
| NUMBER OF SEQ ID NOS: 89 |
| SOFTWARE: FASTERO FOR Windows Version 4.0 |
| SEQ ID NO 3 |
| SEQ ID NO 3 |
| CONTACT |
| CON
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Sequence 74, Application US/10117937

Sequence 74, Application US/10117937

Publication No. US20030220239A1

GENERAL INFORMATION:
APPLICANT: CIL IMMUNO THERAPIES CORP.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
CURRENT APLICATION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/0/117, 937
CURRENT APPLICATION NUMBER: US 60/282,211

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR SEQ ID NOS: 602

NUMBER OF SEQ ID NOS: 602
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Best Local Similarity 100.
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Matches 13; Conservative
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US-10-117-937-74
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Publication No. US20030175250A1

GENERAL INFORMATION:
APPLICANT: JAGER, Elke
APPLICANT: GAGER, Elke
APPLICANT: GAJER, Elke
APPLICANT: GAJER, Elke
APPLICANT: GAJER, Elke
APPLICANT: GOJER, Elve
APPLICANT: GOJER, Elve
APPLICANT: MUMBER, US/A,614
CURRENT FILING DATE: 2003-02-24
PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE PATENT VERSION 3.2
SEQ ID NO 14
LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION BINDING DOMAIN-IMMUNGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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      100.0%; Score 68; DB 4; Length 180; 100.0%; Pred. No. 0.37; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 68; DB 4; Length 18; Pred. No. 0.37; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
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100.0%;
Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                   1 AARASGPGGGAPR 13
                                                                                                                                                                                      50 AARASGPGGGAPR 62
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-207-655-71
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LENGTH: 180
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US-10-188-832-139
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LENGTH: 180
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                                                                                                  APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Glabberg, Wendy M.
APPLICANT: Glabberg, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Marray, Richard
APPLICANT: Watson, Susan R.
ITILE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer CURRENT ELING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR PELLOATION NUMBER: US 60/35,027
CURRENT APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-13
PRIOR PELLOATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR PELLOATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-15
PRIOR PELLOATION NUMBER: US 60/334,393
PRIOR PELLOATION NUMBER: US 60/334,393
PRIOR PELLOATION NUMBER: US 60/334,394
PRIOR FILING DATE: 2001-11-21
PRIOR PELLOATION NUMBER: US 60/347,211
PRIOR PELLOATION NUMBER: US 60/347,319
PRIOR PELLOATION NUMBER: US 60/347,319
PRIOR PELLOATION NUMBER: US 60/347,319
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR PELLOATION NUMBER: US 60/347,319
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR PELLOATION NUMBER: US 60/355,714
PRIOR FILING DATE: 2002-01-08
PRIOR PELLOATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-08
PRIOR PELLOATION NUMBER: US 60/356,714
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SOFTWARE: PatentIn Ver. 2.1
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Publication No. US20040054137A1

GENERAL INPORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT FILING DATE: 2003-08-04

PRIOR PLICATION NUMBER: US/10/296,734

PRIOR PLING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 832
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Matches 13; Conservative 0; Mismatches
                      Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 139, Application US/10188832

Sequence 139, Application US/10188832

Sequence 139, Application No. US20040076955A1

GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Aiz, Matasha
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cencer, Compositions
TITLE OF INVENTION: Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US 60/302,814
PRIOR PELLING DATE: 2001-07-03
PRIOR PELLING DATE: 2001-08-03
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-13
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Publication No. US20040132088A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK.02C1
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT FILING DATE: 2004-02-10
PRIOR FILING DATE: 2002-11-07
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                                                                                                                                                                                                                   Score 68; DB 4; Length 180;
Pred. No. 0.37;
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                                                                                                                                                                                                                                                                                               Indels
                                                                                                           ; OTHER INFORMATION: NYNSO1a consensus polypeptide US-10-296-734-832
                                                                                                                                                                                                                       Query Match
100.0%; Score 68; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 13; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Artificial
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Gaps
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                                                                                                                                                                                                                                                                                     RESULT 15
US-10-657-022-74

| Sequence 74, Application US/10657022
| Publication No. US20040180354A1
| GENERAL INFORMATION:
| APPLICANT: Simard, John J. L. |
| APPLICANT: Diamond, David C. |
| APPLICANT: Liu, Liping |
| TITLE OF INVENTION: EPITOPE SEQUENCES |
| TILE REFERENCE: MANKK. 032A |
| CURRENT APPLICATION NUMBER: 06/409123 |
| PRIOR APPLICATION NUMBER: 60/409123 |
| PRIOR APPLICATION NUMBER: 60/4
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                                                                          1 AARASGPGGGAPR 13
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-657-022-74
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LENGTH: 180
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Gure, Ali, Old, Lloyd, Ritter, Gerd
Gure, Ali, Old, Eloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CLUSES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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COUNTRY: USA
ZIP: 10158
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: Word
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-3au-2004
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION: 530
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 180;
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/165,546D FILING DATE: 02-OCT-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/75,182
FILING DATE: OCTODER 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 FIETh Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 68;
100.0%; Pred. No.
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SSCTWARE: PastSEQ, for Windows Version 4.0
LENGTH: 180
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US-10-751-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 180 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapien
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March 13, 2006, 19:54:06; Search time 8.87059 Seconds (without alignments) 40.793 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161667 seqs, 27834885 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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68
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TOKWATO

ion	e 7, Appli	28	-	205		e 22333, A	e 22332, A	2380	e 3295, Ap	e 16, Appl		e 35, Appl	272	e 641, App	2304		e 4, Appli	9		58,	7, 2	33	e 66, Appl	34,	3763
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-11-155-288-7	US-11-021-441-28	US-10-623-155-496	US-11-096-568A-20556	US-11-096-568A-22334	US-11-096-568A-22333	US-11-096-568A-22332	US-11-096-568A-23806	US-11-072-512-3295	US-11-109-156-16	US-11-096-568A-26217	US-10-531-036-35	US-11-096-568A-27265	US-11-096-568A-641	US-11-096-568A-23045	US-11-096-568A-10542	US-11-110-424-4	US-11-087-099-6009	US-11-100-640-26	US-11-108-528-58	US-11-179-958A-2	US-11-072-512-3369	US-11-037-243-66	US-11-143-980-34	US-11-087-099-3763
DB	7	7	9	7	7	7	7	7	2	7	7	9	7	7	7	7	7	7	7	7	2	_	7	7	7
Length	180	240	20	306	353	358	420	134	678	379	558	974	413	162	249	167	119	268	306	365	537	555	953	280	291
% Query Match	100.0	100.0	82.4	69.1	69.1	69.1	69.il	67.6	66.2	64.7	64.7	64.7	63.2	61.8	61.8	61.0	60.3	60.3	60.3	60.3	60.3	60.3	60.3	9.69	58.8
Score	89	68	26	47	47	47	47	46	45	44	44	44	43	42	42	41.5	41	41	41	41	41	41	41	40.5	40
Result No.	1	7	٣	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 7762, Ap Sequence 20715, A Sequence 2722, Ap Sequence 22508, A Sequence 58, Appl	1 H W (1 L) H C	sequence 18221, A Sequence 18, Appl Sequence 3, Appl Sequence 18, Appl Sequence 18, Appl Sequence 11, Appl Sequence 38, Appl Sequence 38, Appl
US-11-087-099-7762 US-11-096-568A-20715 US-11-072-512-2722 US-11-096-568A-22508 US-11-240-769-58	US-10-92-577-8 US-10-92-577-8 US-11-50-92-577-8 US-11-223-294-54 US-11-205-568-18223	US-11-096-268A-18221 US-11-096-785-18 US-11-056-346-63 US-11-056-346-63 US-11-072-175-184 US-11-072-175-184 US-11-072-175-184 US-11-072-179-38
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1832 178 213 228 233 233	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	496 496 618 618 618 662 736 830 830
58.8 57.4 57.4 57.4 6.7 6.7	70.00.00.00.00.00.00.00.00.00.00.00.00.0	
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26 27 29 30	1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	, E E 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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US-11-096-568A-22334
US-11-096-568A-22334
Sequence 22334, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: US/11/096,568A
CURRENT APPLICATION UNDMER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22334
LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22333, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrow, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: LASTO-1592P025

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22333

LENGTH: 358
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                Length 306;
                                                                                                                                                                                                                                                                 2; Indels
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                       NAME/KEY: misc_feature

; LOCATION: (1)...(306)

; OTHER INFORMATION: Ceres Seq. ID no. 12383286

US-11-096-568A-20556
                                                                                                                                                                                                                Score 47; DB 7
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | NAME/KEY: misc_feature
| LOCATION: (1)..(1553)
| JOCHER INFORMATION: Ceres Seq. ID no. 12408544
| US-11-096-568A-22334
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays subsp. mays
                               TYPE: PRT ORGANISM: Zea mays subsp. mays
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69.28;
                                                                                                                                                                                                                   69.1%;
81.8%;
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Best Local Similarity 69.2%;
Matches 9; Conservative
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                                                                                                                                                                                             Query Match
Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                                                                                         91 ARADGPGTGAP 101
                                                                                                                                                                                                                                                                                                               2 ARASGPGGGAP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-096-568A-22333
         LENGTH: 306
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US-11-096-568A-20556
US-11-096-568A-20556
Sequence 20556, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Marc W.
APPLICANT: Fanger, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21011.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICATION NUMBER: US/10/623,155
CORPRESE FREESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 68; DB 7; Length 240; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.4%; Score 56; DB 6; Length 20;
100.0%; Pred. No. 0.063;
iive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR PILING DATE: 2004-06-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR PILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-06-30
SOFTWARE: PESESSE OF WINDOWS VERSION 4.0
SOFTWARE: PSESSE OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-623-155-496
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LENGTH: 20
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                              APPLICANT: TAMECHIKA, ICHERO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: O'SCHIKAMA, TSUTOMU
APPLICANT: O'SCHIKAMA, TSUTOMU
APPLICANT: O'SCHIKAMA, TSUTOMI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHHO
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US 11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PILING DATE: 2005-03-07
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
SED ID NO 3225
LENGTH: 678
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CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
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PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
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; Sequence 16, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
                 SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                                       ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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80.0%;
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Jun-Ichi Yamamoto
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Tomoyasu Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.v
                                                                                                                                                                                                         OTSUKA, KAORU
NAGAI, KEIICHI
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Jun-Ichi Nezu
                                                                                                                                                                                                                                                 IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RASGPGGGAP 12
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-072-512-3295
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                             Sequence 2332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
FAPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22332
LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 420;
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| LOCATION: (1)...(420)
| JOCHER INFORMATION: Ceres Seq. ID no. 12408542
| US-11-096-568A-22332
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; LOCATION: (1)..(134)
; OTHER LIONEMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
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ORGANISM: Zea mays subsp. mays
                                                                               113 AARGQGPGGEQPR 125
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                                        1 AARASGPGGGAPR 13
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Matches 9, Conservative
  9; Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                US-11-096-568A-22332
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Matches
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US-11-096-568A-27265

Sequence 27265, Application US/11096568A

Sequence 27265, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theory
FILE REFERENCE: 2750-1592PUS

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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US-11-096-568A-641

Sequence 641, Application US/11096568A

Sequence 641, Application US/11/096,568A

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION UNDER: US/11/096,568A

CURRENT APPLICATION UNDER: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 641
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Pred. No. 49;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 6; Length 974;
Pred. No. 76;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1). (413)
OTHER INFORMATION: Ceres Seq. ID no. 15180691
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: EP 02024747.4
PRIOR PILING DATE: 2002-11-06
PRIOR FILING DATE: 2002-10-02
PRIOR PILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: EP 02022880.5
PRIOR APPLICATION NUMBER: BP 02022880.5
PRIOR FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 3.7
SOFTWARE: Patentin version 3.3
SEQ ID NO 35
LENGTH: 974
TYPE: PRT
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ORGANISM: Zea mays subsp. mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Best Local Similarity 71.4%;
Matches 10; Conservative
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Matches 8; Conservative
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US-10-531-036-35
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US-11-096-568A-26217
US-11-096-568A-26217
US-11-096-568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION:

TITLE OF INVEN
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Pred. No. 33;
0; Mismatches 4; Indels
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i LOCATION: (1)..(558)
cother information: Ceres Seq. ID no. 13498878
US-11-096-5688-26217
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR PILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SEQ TO NO 16
LENGTH: 379
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Best Local Similarity 69.2%;
Matches 9; Conservative
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US-11-109-156-16
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Sequence 20165, Application US/11096568A

Publication No. US20060048240A1

ADMINISTRATION

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

ENGINE: 2045

LENGTH: 249
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NAME/KEY: misc feature

LOCATION: (1).7(249)

OTHER INFORMATION: Ceres Seq. ID no. 12411110
US-11-096-568A-23045
; LOCATION: (1)..(162)
; OTHER INFORMATION: Ceres Seq. ID no. 12635935
US-11-096-568A-641
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                                                                                                                                                            1 AARASGPGGGAP 12
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41 AARSGGGGGRP 52
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US-11-096-568A-23045
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March 13, 2006, 18:52:59; Search time 90.3529 Seconds (without alignments) $8.355 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

SUMMARIES	Description	Aay06065 Human can	Aav06064	Aay05986 Human		Aay05979	Aau85105	Adk68648 Epitope	Aaw62584	haw69665 Human NY	Aay05965	•		Aab03154 Human oes	Aab69946 Human NY-	Aag67164 Amino aci		Aae07714	Aau84818	Aaul1543	Abr58672	Abr48210 Human bla	Abu56508 Lung canc	Abu56694	00176116
SOMM	Ω	AAY06065	AAY06064	AAY05986	AAY05978	AAY05979	AAU85105	ADK68648	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164	AAU01535	AAE07714	AAU84818	AAU11543	ABR58672	ABR48210	ABU56508	ABU56694	APD74199
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100
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		4	100.0	180	6	ADW44353	Adw44353 Human aut	
		4	100.0	180	6	ADY85096	Ady85096 Tumor ant	
		4	100.0	180	6	ADZ28913	Adz28913 NY-ESO-1	
		4	100.0	180	σ	ADZ42374	Adz42374 Immunogen	
		4	100.0	180	σ	AEA35651	Aea35651 Human NY-	
		4	100.0	240	σ	ADW99402	Adw99402 NY-ESO-1/	
	45 64	4	100.0	240	0	AEB80047		
						N T CANAGAMIC		
						ALLGNMENTS		
RESULT AAY060 ID A	RESULT 1 AAY06065 ID AAY06065 standard; peptide; 12	g	:andard;	pepti	de;	12 AA.		
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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; parcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic T lymphocyte; CIL. Human cancer antigen NY ESO-1/CAG-3 peptide. (first entry) 16-AUG-1999 AAY06065; 

WO9918206-A2 Homo sapiens 15-APR-1999. 98WO-US019609. 97US-0061428P. 21-SEP-1998; 08-OCT-1997; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Wang RF, Rosenberg SA;

Cancer antigen NY ESO1/CAG-3. WPI; 1999-277270/23.

Example 11; Page 50; 88pp; English.

This peptide corresponds to amino acid residues 51-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HIA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; loung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; parcreatic cancer; liver cancer; parcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                       Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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                                                      AAY05986 standard; peptide; 14 AA.
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cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                  Score 64; DB 2; Length 12; Pred. No. 0.049;
                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                    Human cancer andigen NY ESO-1/CAG-3 peptide.
                                                                                               0; Mismatches
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                                                                                                                                                                                                                     AAY06064 standard; peptide; 13 AA.
                                                                  Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                          16-AUG-1999 (first entry)
                                                                                                                         1 ARASGPGGGAPR 12
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                                         Sequence 12 AA;
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The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CaG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their CC variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cranspanic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or inhibiting cancer by administering a cancer peptide. With or without an HIAA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, corrorma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is return to a patient
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100.0%; Pred. No. 0.056;
ive 0; Mismatches 0; Indels
Claim 25; Page 50; 88pp; English.
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Matches 12; Conservative
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RESULT 4

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AAY05978;

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The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CMG-3 (or CMG-3) ORF1 (see AAY05965), and wand potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 3) ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 3) ORF2 (see AAY05966), portions of the cancer rank protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide. The cancer bedtides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cerrical cancers blander cancer, liver cancer, leukaemia, uterine cancer, cerrical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                              NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 64; DB 2; Length 20; 100.0%; Pred. No. 0.076; ive 0; Mismatches 0; Indels
                                                          Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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        (first entry)
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1es 12; Conservative
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        16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                     vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAV05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF2 (see AAV05966), portions of them and their cancer recines that protect against cancer. The invention provides vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen, antibodies reacting with a CAG-3 cancer peptide or tumour antigen, antibodies reacting with a CAG-3 cancer peptide or inhibiting cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carvoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, particula cancer, bladaloma is traated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                  NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leuksemia, non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; errical cancer; bladder cancer; kidney cancer; pancial cancer; liver cancer; bladder cancer; kidney cancer; pancialic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine.
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                                                                                                                                                                Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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AAY05978 standard; peptide; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US019609.
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                                                                                                         16-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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Query Match

Matches

8 셤 AAY05979

RESULT 5 AAY05979 Epitope liberation-related NY-ESO-1 protein SeqID11.

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The invention rélates to a new synthetic polypeptide (I) comprising several different relationship relative to their linked coerner relative to their linked in the parent polypeptide to impede, abrogate or otherwise alter at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides. The synthetic polypeptides and polymelocides or saynthetic polypeptides. The synthetic polypeptides and polymelocides or a savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, osesophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HVV (human immune immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Ce almonatia, streptococcal, Legionella and Mycobacterium or paraaitic (e.g., infections caused by plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
             Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 27; 364pp; English.
                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                                                                 25-MAY-2001; 2001WO-AU000622
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                                                                                                                                                                                                                                                                                                                                                                              Ramshaw IA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen or cancer.
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                                                                                                                                                                 WO200190197-A1.
                                                                                                                                                                                                                                                                                                                                                                            Thomson SA,
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This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate polypeptide sequence including the epitope, wherein the substrate processing by a proteasome, contacting the substrate with a composition including the proteasome, and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, proteasoide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation, where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine (CTL) to be used in adoptive immunotherapy. The invention is also useful cor the knowledge that such epitopes are, in fact, produced by the virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic cor the host. The present sequence is that of a protein which is related to
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                               epitope liberation; substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 11; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qiu Z,
                                                                                                                                                                                                                                                                             07-NOV-2002; 2002US-00292413.
                                                                                                                                                                                                                                                                                                                   07-NOV-2001; 2001US-0336968P.
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                                                                                                                                                                                                                                                                                                                                                          (SIMA/) SIMARD J J L.
(DIAM/) DIAMOND D C.
(QIUZ/) QIU Z.
(LEIX/) LEI X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-167209/16.
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wes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 179 AA;
                                                                                                                                                                                                US2003228634-A1.
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                       11-DEC-2003.
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Matches
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ID AAW6
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Gaps

Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

Homo sapiens WO9832855-A1

formerly known as LL-1.2 clone.

Human NY-ESO-1 protein sequence,

(first entry)

27-0CT-1998

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of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression
                                                                                                                                                                                                  Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Old LJ, Jager E, Knuth A;
                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "potential myristorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "potential myristorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                               Cancer associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scanlan M, Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US016335,
                                                               (first entry)
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N-PSDB; AAV38566.
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                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drijfhout JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1997;
                                                               17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09814464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1998
AAW62584;
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New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours.

Example 2; Page 57-58; 73pp; English.

Boon-Falleur T;

Godelaine D,

De Smet C,

WPI; 1998-427951/36. Lethe B, Lucas S,

N-PSDB; AAV50348

(LUDW-) LUDWIG INST CANCER RES

27-JAN-1997;

98WO-US001445. 97US-00791495.

27-JAN-1998;

30-JUL-1998.

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The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an imunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an imunogenic fragment to ameliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells opecific for a LAGE-1 TAP comprising contexting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an expression prosecting a lagent presenting a complex of a LAGE TAP or an expectively enriching a population of T cells with a lagent presenting a complex of a LAGE TAP or an expective to the subject of the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting a complex of a LAGE TAP or an expective to the lagent presenting 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
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Gaps ö

100.0%; Score 64; DB 2; Length 180; 100.0%; Pred. No. 0.51; ive 0; Mismatches 0; Indels

llarity 100.0%; Conservative

Query Match Best Local Similarity

12;

Best Loca Matches

1 ARASGPGGGAPR ARASGPGGGAPR

ઠે 유 AAW69665 standard; protein; 180 AA.

AAW69665 ID AAW6 XX RESULT 9

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158.
                    Homo sapiens.
Unidentified.
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                                                                   Peptide
                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                           Peptide
The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and content tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portfons of these peptides comprising ORF1, ORF2 (see CAY05966), portfons of these peptides and their variants (see AAY05965-CC AAY05966), portfons of these peptides and their variants (see AAY05965-CC AAY05966), portfons of these peptides that intent from development of cancer. The invention provides: vectors and host cells a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods of tor preventing or inhibiting ancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, concerned, protected to metastatic melanoma, thymoma, conversing the cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, broaten, pancreatic and thyroid cancers. Melanoma is transfer or period. The cancer peptide in vitro for subsequent
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       non-Hodgkins lymphoms, Hodgkins lymphoms, lung cancer; metastassis; melanoma; adenocarcinoma; thymoms; colon cancer; uterine cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytotoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 2; Length 180;
Pred. No. 0.51;
0; Mismatches 0; Indels
                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY52430 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                       Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                   98WO-US019609
                                                                                                                                                                         97US-0061428P
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Best Local Similarity 100....

Best 12; Conservative
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(first entry)
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                                                                                                                                                                                                                        Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARASGPGGGAPR
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                                                                                                                                                                                                                                             WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           return to a patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 180 AA;
                                                                                Homo sapiens
                                                                                                     WO9918206-A2.
                                                                                                                                                                         08-OCT-1997;
                                                                                                                                                   21-SEP-1998;
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15-FEB-2000
                                                                                                                            15-APR-1999
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Class I HLA-A24 and HLA-
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                                                                                                                                                                                                                                                                                                                 'note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .92
:e= "Peptide presented by MHC Class I HLA-B7, HLA-B8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .96
.e= "Peptide presented by MHC Class I HLA-B44"
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note= "Peptide presented by MHC Class I HLA-B52"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC Class I HLA-A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Peptide presented by MHC Class I HLA-A3"
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note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                              "Peptide presented by MHC Class I HLA-Al"
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                                                                                                                                                                                                                                                                                                                                                                           "Peptide presented by MHC Class I HLA-Al"
                                                                                                                               "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                    "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                         HLA-B7"
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hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           presented by MHC Class I
                                                                                                                                                                                                                          .72
e= "Peptide presented by MHC Class I
                                                                                                                                                                                                         "Peptide presented by MHC Class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presented by MHC Class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC Class
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Peptide presented by
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                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Peptide
                                                                                                                                                                                                                                                                                                                                         and HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .116
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Peptide Peptide

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the CAMEL (Cytotoxic T lymphocyfes (CTL) recognised Antigen on MELanoma) protein, a tumour-asociated antigen. The tumour-associated antigen displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogentc peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading frame (ORF) -1 that contain epicopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma; melanoma; ovary; testis; transmembrane domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 3; Length 180; 100.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Potential N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ....
                                                                                                                                                                                                                                            (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
(UYHO-) UNIV HOSPITAL LEIDEN.
                                                                                                                                                                                                                                                                                                                     Heider K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 62-63; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB03154 standard; protein; 180 AA.
                                                                                                                                                 99WO-EP007832
                                                                                                                                                                                               98EP-00119583
                                                                                                                                                                                                                                                                                                                     Schrier PI, Aarnoudse CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-339685/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD00152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion proteins
                                                    WO200023584-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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       Homo sapiens
                                                                                                                                                 15-OCT-1999;
                                                                                                                                                                                               16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                  27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB03154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer CDNA library. Tissue, localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY -ESO-1 are bound by both MHC (major histocompatibility complex) Class I and Class I HIA-A2 molecules, thereby stimulating color of cytocoxic T-cells, while peptides AAYS2435-YS2440 bind to Class II HIA-DESO-1 may be used in methods and color the treatment, diagnosit and prevention of cancers compositions used for the treatment, diagnosis and prevention of cancers compositions used for the treatment, diagnosis and prevention of cancers compositions used for the treatment, diagnosis and prevention of cancer lund as melanoma. Dreast cancer lund cancer lund cancer lund selectives and cancer lund cancer lund selectives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                      Chen Y, Scanlan M, Alexander K, Old LJ;
                                                                   /note= "Peptide presented by MHC Class I HLA-B52"
159. .167
'note= "Peptide presented by MHC Class I HLA-A3"
62. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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hea 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ovarian cancer, thyroid cancer, bladder
stimulate the proliferation of T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70862 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 30; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                98US-00062422.
98US-00165546.
                                                                                                                                                                                                                   99WO-US006875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Stockert E, Jager B,
Gure A, Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-038483/03.
N-PSDB; AAZ38380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180 AA;
                                                                                                                   WO9953938-A1
                                                                                                                                                                                                                                                                   17-APR-1998;
                                                                                                                                                                                                                                                                                       02-OCT-1998;
                                                                                                                                                                28-OCT-1999
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AAY70862;

Query Match

Best Loca Matches

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Gaps

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protein

Klade C;

Chen Y, Scanlan M;

Knuth A,

old LJ,

CANCER RES

99US-00359503

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(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                (SLOK ) SLOAN KETTERING INST C (CORR ) CORNELL RES FOUND INC.
                                                                               14-JUL-2000; 2000WO-US019220.
                                                                                                                                                                                        Jager E, Stockert E,
                                                                                                                                                                                                                   2001-182822/18.
                                                                                                                                                                                                                             N-PSDB; AAF58634.
                          WO200107917-A1
 Homo sapiens.
                                                                                                          23-JUL-1999;
                                                     01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a CDNA ilbrary propared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The antigenic sequences in the N-terminal half of the protein. The antigenic sequences in the N-terminal half of the protein. The antigenic and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to oesophageal cancer.

Can also be used to generate diagnostic or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                         New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions. e.g. infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                           Sahin U, Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 64; DB 3; Length 180; Best Local Similarity 100.0%; Pred. No. 0.51; Matches 12; Conservative 0; Mismatches 0; Indels
       /note= "Potential O-phosphorylation site"
138
                                       /note= "Potential O-phosphorylation site"
                                                    152. .172
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                         Scanlan M, Gure AO, Chen Y, Tureci O, Old LJ;
                                                                                                                                                                                                    KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB69946 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 3; 9pp; English.
                                                                                                                                                                                                  (SLOK ) SLOAN KETTERING INST CF
(CORR ) CORNELL RES FOUND INC.
(LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                98US-00013150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                 WPI; 2000-410880/35.
N-PSDB; AAA61483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180 AA;
Modified-site
                         Modified-site
                                                                                                                                                26-JAN-1998;
                                                                                                                                                                           03-OCT-1996;
                                                                                          US6069233-A
                                                                                                                     30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB69946;
                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                     e.g.
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Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 64; DB 4; Length 180; 100.0%; Pred. No. 0.51; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG67164 standard; protein; 180 AA.
                                                                                                                                                                                       Example 5; Fig 3; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-2001; 2001WO-US002126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000; 2000US-00510635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200162917-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG67164;
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Lethe B, Boon-Falleur T;

XX

WPI, 2001-550091/61.

DR N-PSDB, AAH75118.

XX

WPI, 2001-550091/61.

DR N-PSDB, AAH75118.

XX

Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful for diagnosing testicular tumors.

YX

XX

Genomic sequence represents cancer testis tumour antigen NY-ESO-1

CC dlso called LAGE-2). NY-ESO-1 is a molecule that is processed to at class I and class II and/or historocompatibility complex (WHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, cc class I and class II and/or historocompatibility complex (WHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, cc liver or brain tissue. The presence or level of expression of NY-ESO-1

XX

CC may be assayed for the diagnosis of cancer, especially testis tumours XX

Sequence 180 AA;
```

Search completed: March 13, 2006, 19:03:59 Job time: 90.3529 secs

ö

0; Gaps

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 13, 2006, 19:04:24 ; Search time 14.2588 Seconds (without alignments) 80.975 Million cell updates/sec

US-09-529-206E-29 64

1 ARASGPGGGAPR 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq lengt; 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR_80:* Database

1: pirl: * 2: pir2: * 3: pir2: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	CREB-binding prote			ס	hypothetical prote		ε	conserved hypothet	conserved hypothet		H+-transporting tw	XAA-PRO aminopepti	hypothetical prote		steroid hormone re	KIAA0641 protein -	ATP dependent DNA	acclimation protei	hypothetical prote		MAP kinase 3 (EC 2	hypothetical prote	н	androgen receptor	androgen receptor	androgen receptor	regulatory protein	collagen alpha 1 c	hypothetical prote
		ai		T36874	G72663	T36115	T29031	\$50754	C87425	T36104	G75580	AB3648	804673	F82878	T39312	868518	A29345	T00378	T35694	T04476	T36712	S08341	A48082	A86182	S02165	A34721	B34721	A39248	A87431	A36226	C72683
		g :	7	~	N	~	N	~	~	~	7	~	~	7	~	~	7	~	~	7	~	N	Н	~	~	~	~	~	~	~	~
		Length	3190	185	201	222	327	351	378	436	474	173	286	357	371	505	521	1207	1690	82	290	335	379	383	679	910	911	919	954	730	103
æ	Query	Match	68.8	9.59		Š.	9.59	9.59	9.59	65.6	9.59	64.1	64.1	64.1	64.1	64.1	64.1	64.1	64 .il	62.5				ä				62.5	ď	61.7	6.09
	,	Score	44	42	42	42	42	42	42	42	42	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40	40	40	40		39
	Result	. No.	-	7	m	4	Ŋ	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

Pur beta - human (	competence/damage-	histocompatibility	hypothetical prote	polygalacturonase	DNA-invertase - Rh	probable transcrip	transcription acti	polygalacturonase	hypothetical prote	hypothetical prote	Ca2+/calmodulin-de	Ca2+/calmodulin-de	endopeptidase Clp	polygalacturonase	polygalacturonase
B45036	E87464	900691	T35619	S25825	S42585	F95899	A47008	S25824	B72677	S55626	S28184	JC1451	T52451	830067	830066
~	N	7	N	~	7	~	~	7	~	7	7	~	7	7	0
114	163	166	187	197	213	260	269	306	307	349	377	380	387	410	410
6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09	6.09	60.09	6.09	6.09	6.09	60.9
_				_	_	_	σ.	σ	φ	σ	•	σ.	6	σ	_
39	39	39	39	39	35	ñ	m	m	m	m	3,	m	3	m	39

## ALIGNMENTS

```
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13828
R.Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G. Nature 386, 735-738, 1997
A.Ritle: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A.Reference number: Z17785; MUID:97263578; PMID:9109493
A.Accession: T13828
A.Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>
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: | | | | | | | | 320 NGPGGGGPR 328 4 SGPGGGAPR 12 g ઠે

RESULT 2

hypothetical protein SCI51.11c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: Streptomyces coelicolor
C;Date: 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36874
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Bubmitted to the EMBL Data Library, August 1999
A;Reference number: Z21617
A;Accession: T36874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-185 <MUR>
A;Cross-references: UNIPROT: Q95229; UNIPARC: UPI00000DB31A; EMBL: AL109848; PIDN: CAB52835
C;Genetics:

A; Gene: SCOEDB:SCI51.11c

ö Gaps ; Query Match 65.6%; Score 42; DB 2; Length 185; Best Local Similarity 80.0%; Pred. No. 50; Matches 8; Conservative 0; Mismatches 2; Indels

1 ARASGPGGGA 10

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Gaps

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C;Accession: $50754
R;Woessner, U.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring, Blol. 26, 947-960, 1980
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: $50754; MUID:95093034; PMID:8000007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon, W.C.; Feldblyum, T.V.; Paulsen, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 «STIO»
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; P
                    A;Molecule rype: DNA
A;Molecule rype: DNA
A;Residues: 1-327 «WUX»
A;Cross-references: UNIPROT:001799; UNIPARC:UPI0000078FFF; EMBL:AF003139; PIDN:AAB54156.
A;Experimental source: strain Bristol N2; clone F53G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q39492; UNIPARC:UP100000A170A; EMBL:L29028; NID:g530877; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 351;
                                                                                                                                                                                                                                                                                    Length 327;
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                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aldose 1-epimerase [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                 DB 2;
81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
86;
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Pred. No. 91;
1; Mismatches
A, Status: preliminary, translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein WP6 - Chlamydomonas eugametos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.6%;
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C;Superfamily: aldose 1-epimerase
                                                                                                                                                                                                                                                                                    65.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                A,Gene: CESP:F53G12.7
A,Map position: 1
A;Introns: 59/3; 138/1; 223/2
                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AEAAGGGGGAP 123
                                                                                                                                                                                                                                                                                                                                                                                                1 ARASGPGGGAP 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 NGPSGGAPR 290
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-351 <WOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S50754
                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics
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                                                                                                                                                                                                                                                 C;Accession: G72663
R;Kawarabayasi, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takah
bNA, Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUD:99310339; PMID:10382966
A;Accession: G72663
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-201 «KAW»
A;Cross-references: UNIPROT:Q9YE35; UNIPARC:UPI000005DC7C; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain Kl
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rimurphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBt Data Library, April 1999
A;Reference number: 221597
A;Accession: T36115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-222 <MUR>
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Genetics:
A,Gene: SCOEDB:SCE15.12c
C;Superfamily: NAD(F)H-dependent FMN reductase (sulfate starvation-induced protein 4);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                Species: Aeropyrum pernix
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Accession: G72663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable oxidoreductase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004 C;Accession: T36115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F53G12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.6%; Score 42; DB 2; Length 201; Best Local Similarity 75.0%; Pred. No. 54; Matches 9; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.6%; Score 42; DB 2; Length 222; Best Local Similarity 72.7%; Pred. No. 59; Matches 3; Indels Matches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: APE0734
C;Superfamily: Aeropyrum pernix hypothetical protein APE0734
                                                                                                                                                                   hypothetical protein APE0734 - Aeropyrum pernix (strain Kl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T29031
R; Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A; Description: The sequence of C. elegans cosmid F53G12.
A; Reference number: Z20555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 ARASGVGGRRPR 48
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A; Accession: T29031
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Gaps

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A;Molecule type: DNA
A;Residues: 1-173 «KUR»
A;Residues: 1-173 «KUR»
A;Residues: 1-173 «KUR»
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UP10000058740; GB:AE008918; PIDN:AAL54349.1
A;Experimental source: strain 16M
A;Experimental source: strain 36M
A;Gene:BWEIL1107
A;MAP position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica C;Species: Rhodopseudomonas blastica C;Species: Rhodopseudomonas blastica C;Date: 07-Sep-1990 #text_change 31-Dec-2004 C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription. A;Reference number: S04666; MUID:8508188; PMID:6209404
A;Reference number: S04666; MUID:8508188; PMID:6209404
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;bate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Bubmitted to Genbank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mixA;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-357 <GLA>
A,Cross-references: UNIPARC:UP10000C1CAC; GB:AE002152; GB:AF222894; NID:G6899532; PIDN
A,Experimental source: serovar 3; blovar 1
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A; Residues: 1-286 <TYB>
A; Cross-references: UNIPROT: PD5436; UNIPARC: UPI0000126582
C; Superfamily: H(+)-transporting ATP synthase gamma chain
C; Kcywords: ATP biosynthesis; hydrolase; membrane-associated complex
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                                                                                                                                                                                                                                                                                                                Length 173;
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66;
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Pred. No. 99;
0; Mismatches
                                                                                                                                                                                                                                                                                                        64.1%; Score 41; DB 100.0%; Pred. No. 66; iive 0; Mismatches
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A,Genetic code: SGC3
C,Superfamily: X-Pro aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.1%;
80.0%;
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Best Local Similarity 80.00,
Best Local Similarity 80.00,
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Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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A; Status: preliminary
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S04673
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R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999.
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A.Reference number: A75250; MuID:20036896; PMID:10567266
A.Accession: G75580
A.Acces
                                                                                                                                                                                                                                                                                                                                A;Reference number: Z2157
A;Recession: T36104
A;Accession: T36104
A;Accession: T36104
A;Accession: T36104
A;Accession: T36104
A;Accession: T36104
A;Residues: 1-436 cMUR>
A;Residues: 1-436 cMUR>
A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UP1000017AD99; EMBL:AL049707; PIDN:CAB41270.
C;Genetics:
A;Gene: SCOEDB:SCE15.01
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Accession: AB3648
                                                                                                                                                                                                                C,Accession: T36104
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flagellar basal-body rod protein flgf [imported] - Brucella melitensis (strain 16M)
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                                                                                                                - Streptomyces coelicolor (fragment)
                                                                                                            conserved hypothetical protein SCE15.01 - Streptomyces coelicolor (fragment)
C,Species: Streptomyces coelicolor
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0821
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Pred. No. 1e+02;
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Les 8; Conserv
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Gaps

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A; Residues: 1-521 «GIO»

A; Residues: 1-521 «GIO»

A; Cross-references: UNIPARC: UNIPARC: UDIO000142399; EMBL; X51416; NID: g36608; PIDR

B; Wiley, S. R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.

Genes Dev. 7, 2206-2219, 1933

A; Title: SV40 early-to-late switch involves titration of cellular transcriptional representation: A49074

A; Reference number: A49074

A; Reference unimber: A49074

A; Status: preliminary

A; Status: preliminary

A; Status: protein type: protein

A; Residues: 166-169, X; J71-173 «MIL»

A; Cross-references: UNIPARC: UPI000017A1DF

C; Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi F; 174-434/Domain: erbA transforming protein homology «ERBA»

F; 176-196/Region: zinc finger
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66.7%; Pred. No. 1.6e+02;
ive 1; Mismatches 3; Indels
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Job time : 14.2588 secs
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Matches 8; Conserv
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S6818; S68519
R;Noben-Trauth, K.; Naggert, J.K.; North, M.A.; Nishina, P.M.
A;Accession: S6818; MUID:96195061; PMID:8606774
A;Accession: S6818; MUID:96195061; PMID:8606774
A;Accession: S6818
A;Status: preliminary; nucleic acid sequence not shown
A;Nolecule rype: mRNA
A;Residues: 1-505
A;Accession: S68519
A;Cossion: S6
                                                                                                                                                      C; Accession: T39312
R; Wood, V. V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A; Reference number: Z21843
A; Accession: T39312
A; Status tyreliminary; translated from GB/EMBL/DDBJ
A; Residues: Lype: DNA
A; Residues: 1-371 < WOO>
A; Residues: 1-371 < WOO>
A; Cross-references: UNIPROT:042905; UNIPARC:UP100001352D5; EMBL:AL022117; PIDN:CAA17929.
C; Genetics:
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C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
C;Accession: A29345; A9074
R;Giquere, V.; Yang, N.; Sequi, P.; Evans, R.M.
Nature 331, 91-94, 1988
A;Title: Identification of a new class of steroid hormone receptors.
A;Reference number: A29345; MUID:88122546; PMID:3267207
                                                                                                                                        Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                               protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
"A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL, Spring databases.
HMD1, AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
NON TER
SEQÜENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
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Last annotation update)
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              Q8NAC4_HUMAN
Q8NZ61_9DELT
Q8ALD1_ORYSA
Q4NTZ7_9DELT
Q70EK5_ANGGA
Q4SW43_TETNG
Q4NWX4_9DELT
Q5NTS5_CANFA
Q63NC9_BURPS
Q63NC9_BURPS
Q62DA7_BURPS
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Q9NY13_;
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NCBI_TaxID=9606;
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97.196 Million cell updates/sec
                                                                                                      March 13, 2006, 18:53:23 ; Search time 87.1059 Seconds
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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CTG1B HUMAN
Q7LBY4 HUMAN
CTAG2 HUMAN
Q63QT8 BURPS
Q62H22_BURMA
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Q96S27_HUMAN
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Int. J. Cancer 82:442-448(1999)
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   Nelson D.L.;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                    Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T., H., a new gene with tumor specificity."; Int. J. Cancer 76:303-908(1998).
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Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
Schwartzentruber D.J., Rosenberg S.A.;
Schwartzentruber D.J., Rosenberg S.A.;
A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames.";
J. Immunol. 161:3596-3606(1998).
-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in utcrine myometrium.
-!- SIMILARITY: Belongs to the CTAG family.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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Pred. No. 0.17;
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Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
Gly-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U87459; AAB49693.1; -; MRNA.
EMBL; AJ003149; CAA05908.1; -; MRNA.
EMBL; AF038567; AAD05202.1; -; MRNA.
                                                                                                                       MEDLINE=98289662; PubMed=9626360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 AA; 17992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
Q7LBY4 HUMAN
ID Q7LBY4_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:2491; CTAG1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 271:93-98(2001).
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                                                           NUCLEOTIDE SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen 1-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPBIAS
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Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
DNA methylation is the primary silencing mechanism for a set of germ "DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an
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Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen E., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
"Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
"Interleukin-2-induced, melanoma-specific T cells recognize CAMEL,
unexpected translation product of LAGE-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS GLN-6; GLN-89 AND ARG-138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 64; DB 2; Length 180; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTAG2 HUMAN STANDARD; PRT; 210 AA. 075638; 075637; 090180; 090189; 090479; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) Cancer/Lestis antigen 2 (LAGE-1 protein) (ESO-2 protein) Name-CTAG2; Synonyme-ESO2, LAGE1; Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lethe B.G.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR277315; AAL27014.1; -; Genomic_DNA.
EMBL; AZ375977; CAB76943.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ARASGPGGGAPR 62
                                                                                                                                                                            Platzer M.;
Submitted (MAY-2001)
                                                                                                                                                                                                                                                                                                                        Platzer M.;
Submitted (JUL-2001)
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Query Match
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                        TISSUE-Placenta;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDETR R.D., Feingold E.A., Grouse L.H., Derge J.G.,

MISCHIL S.P., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

MISCHORL S.P., Jeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

MA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MISCHARG S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

M. Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

M. Helton E., Ketreman M., Madan A., Pourg A.C., Shevchenko Y., Bouffard G.G.,

M. Helton B., C., Garimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

M. Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEM outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MSVWDORREGAGRMRVGWGLGSASPEGGKARDLRTPKHKV
SEQRPGTPGPPPPEGAGGDGCRGVAFNVMFSAPHI -> IR
LTAADHRGLGLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms=2;
Name=LAGE-1B; Synonyms=LAGE-1L;
Isold=075638-1; Sequence=Displayed;
Name=LAGE-1A; Synonyms=LAGE-1S;
Isold=075538-2; Sequence=VSP_004301;
Isold=075538-2; Sequence=VSP_004301;
TISSUE SPECIFICITY: Testis and very low level in placenta and in some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: A transmembrane domain is present in isoform LAGE-1A. SIMILARITY: Belongs to the CTAG family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing; Antigen; Polymorphism; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 1; Length 210;
Pred. No. 2.8;
0; Mismatches 1; Indels
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8BE0EE00AE55E8BE CRC64;
                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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/FTId=VAR_007856.
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EMBL, AJ223093; CAA1116.1; -; Genomic_DNA.
EMBL, AJ223041; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
EMBL, AJ012834; CAA10194.1; -; mRNA.
EMBL, AJ012835; CAA10196.1; -; mRNA.
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Ensembl; ENSG0000126890; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AA; 21120 MW;
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91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     head and neck cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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H-InvDB; HIX0017163; -.
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STRAIN=E896243;

X PubMed=15377794, DOI=10.1073/pnas.0403302101;
A holden Mr.G., Titball R.W., Pacock S.J., Cerdeno-Tarraga A.-M.,
Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
A hilling T., Crossman L.C., Pitt T., Charcher C., Mangall K.L.,
A Brooks K., Brown K.A., Brown N.P., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
A Reltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Rabbinowitsch B., Rutherford K., Sanders M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
Songsivilai S., Stevens C., Barrell B.G., Oyston P.C.F., Parkhill J.;
Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
Michonic plasticity of the causative agent of melioidosis,
                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, pseudomallei group.
NCBI_TaxID=28450;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 23344;
PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
EMBL. BXST1-955; CAH36946.1; -; Genomic_DNA.
GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
GO; GO:0006260; P:DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 2; Length 362; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA; 38726 MW; DSFF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                        Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-007-2004 (TrEMBLrel. 28, Created)
25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerase III, delta subunit (EC 2.7.7.7).
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InterPro; IPR005790; DNA polIII delta.
Pfam; PF06144; DNA pol3_delta; I.
                                                                                                                                    PRT;
                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                  Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR01128; hola; 1.
                                                                                                                        0630T8 BURPS PRELIMINARY;
0630T8;
25-0CT-2004 (TEMBLEEL 28,
25-0CT-2004 (TEMBLEEL 28,
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51 ARASGPRGGAPR 62
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es 10; Conservative
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Altschul S.P., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhart N.R.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhart N.R.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhart N.R.,

And Stage L. Buetow K.H., Schaefer C.F., Bhart N.R.,

A paperon M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carnhori P., Prange C.

Brownstein M.J., Usdin T.B., Toobhyuki S., Carnhori P., Prange C.

Brownstein M.J., Usdin T.B., Toobhyuki S., Carnhori P., Prange C.

Brownstein M.J., Widnin T.B., Toobhyuki S., Carnhori P., Prange C.

Brownstein M.J., Widnin T.B., Toobhyuki S., Carnhori P., Prange C.

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

W. Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

W. Hiller M., Madan A., Young A.C., Shevchenko Y., Bonffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

T. "Generation and initial analysis of more than 15,000 full-length human manner only
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                Gaps
Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.P.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. Uls.A. 101:14246-14251(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                             GO, GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016560; P:DNA replication; IEA.
InterPro; IFR010372; DNA pol3 delta.
InterPro; IFR005790; DNA pol3 delta.
Pfam; PF06144; DNA pol3 delta; 1.
TIGREAMS; TIGR01128; holA; 1.
TIGREAMS; TIGR01128; holA; 1.
SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                            Score 54; DB 2; Length 362;
Pred. No. 9.3;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015174; AAH15174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Q96BUZ;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                    Gaps
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                                       DB 2; Length 194;
19;
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                                                                    Indels
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Submitted (SRP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC013426; AAH13426.1; -; mRNA.
SEQUENCE 896 AA, 94247 MW; ODE6869BCFD4C471 CRC64;
1 1 1 1 94 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;
                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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(TrEMBLrel. 28, Last sequence update)
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Pred. No. 84;
0; Mismatches
                                                                   0; Mismatches
                                         78.1%; Score 50;
                                                      Pred. No.
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81.8%;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                      81.8%;
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D GEDHVE HUMAN PRELIMINARY;
AC GEDHVE;
DT 25-0CT--2004 (TrEMBLrel. 28

DT 25-0CT--2004 (TrEMBLrel. 28
                                                                                                                                                                                              Q96D18_HUMAN PRELIMINARY;
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                    9; Conservative
                                                                                                                         99 ARRQGPGGGAP 109
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                                                                                               1 ARASGPGGGAP 11
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                                                      Local Similarity
                                                                                                                                                                                                                                                                  PLEKHG2 protein.
Name=PLEKHG2;
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                                       Query Match
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RAY COLOURS, DOI-10.11036/NG1242,

RAY MARAMATEN A., Niebikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamaten A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Niebi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Kawai Y., Isono Y., Nakamura Y.,

RA Sinratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E.,

RA Gugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E.,

RA Amazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotura T.,

RA Inose N., Masabhino K., Yuuki H., Oshima A., Saaaki N., Aotsuka S.,

RA Imose N., Matsunawa H., Ichihara R., Takeuchi K., Aira M.,

RA Noriya S., Momiyama H., Satoh N., Takami S., Tersabhima Y., Saroh S.,

RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Matamake K., Kumagai A., Itakura S., Futuzumi Y.,

RA Matamaka K., Fujii Y., Zazaki K., Hirao M., Ohmori Y.,

RA Matsumura K., Nakajima Y., Takino T., Shiqeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinagan A., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Matsumura K., Nakajima Y., Mizura Y., Komiyama M., Sasaki M.,

RA Matsumura K., Nakajima Y., Mizuno T., Matsubima-Sugano J., Satoh T., Shizuti Y., Takahashi Y., Yamashita R.,

RA Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nompa H., Nakamura Y., Ohara O., Isogai T., Sugano S.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

RA Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSG00000090924; Homo sapiens.
HGNC; HGNC:29515; PLEKHG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 36:40-45(2004).
-!- SIMILARITY: Contains 1 PH domain.
EMBL; AKO24429; BAB15719.1; -; mRNA.
HSSP; Q64096; 1KZ7.
                                                       TISSUE=Spleen;
PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEFF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
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InterPro; IPR000219; RhoGEF.
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Pfam; PF00621; RhoGEF; 1.
                           NUCLEOTIDE SEQUENCE
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                      PLEKHG2 protein (Fragment).
Name=PLEKHG2;
Name=PLEKHG2;
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Director MGC Project;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 PH domain.
EMBL; BC075858; AAH75858.1; -; mRNA.
InterPro; IPR001019; PH.
InterPro; IPR001019; RhoGEF.
Pfam; PF00169; PH; 1.
Pfam; PF00611; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1253, AA; 134404 MW; 534EB31283E535C5 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
FLJ00018 protein (Fragment)
Name-PELEKHGZ; Synonyme=FLJ00018;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00233; PH; 1.
SMART; SM00325; RhoGBF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1158 ARROGPGGAP 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 81.8
1es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences.
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                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                  NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaea; Oryza.
                                                                                                                  ö
                                                         78.1%; Score 50; DB 2; Length 1430; 81.8%; Pred. No. 1.3e+02; rive 0; Mismatches 2; Indels
1430 AA; 152528 MW; E4DF0BFDACCB6A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Q5Z8E2;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein P0487E11.17.
                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                   Local Similarity 81.8
Hes 9; Conservative
                                                                                                                                                                      1 ARASGPGGGAP 11
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Teitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tellon L.J., Koo H., Zismann V., Heiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mitc O., Salzberg S.L., Fraser C.M., M., Characken S.S., Salzberg S.L., Fraser C.M., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                              Hypothetical protein 031191_A10.131 (Hypothetical protein 031014_E06.5).
Name=031191_A10.131; Synonyms=031014_E06.5;
Name=031191_A10.131; Synonyms=031014_E06.5;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                        Gramen; QTFIE3; -. GO; GO: 0000151; C: ubiquitin ligase complex; IEA. GO; GO: 0004842; F: metal ion binding; IEA. GO; GO: 0004842; F: ubiquitin-protein ligase activity; IEA. GO; GO: 0008270; F: zinc ion binding; IEA. GO; GO: 0016567; F: zinc ion binding; IEA. InterPro; IPR008700; NOI.
                                                                                                                                                                                                                                                                                                Buell R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00518; ZF RING_1; 1.
PROSITE; PS50089; ZF RING_2; 11.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 49 Aa, 47196 MW; BBEFF7708B292296 CRC64;
                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0063J18.9.
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Pred. No. 84;
1; Mismatches
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Pfam; PF00097; zf-C3HC4; 1.
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                                                                            Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Adki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Ikeno M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K., Machara T., Kitura A., Kobayashi N., Kono I., Nakanita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamura M., A Nagasaki H., Nakashima M., Nakamu Y., Nakamichi Y., Nakamura M., A Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Tarasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Xahoo H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Xano M., Jiang J., Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
Ensembl; RSSG00000165933; Homo sapiens.
Expendical protein.
SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;
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                                                            MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
EMBL; AP003793; BAD53925.1; -; Genomic_DNA.
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SEQUENCE 262 AA; 27141 MW; 816A1189E43BA42A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gene X.
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Pred. No.
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Q96S27;
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Best Local Similarity
NCBI_TaxID=39947;
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RESULT 12
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STRAIN=2CP-C;
STRAIN=2CP-C;
STRAIN=2CP-C;
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Fitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter capachalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                               Anaeromyxobacter dehalogenana 2CP-C.
Bacteria; Proteobacteria; Daltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
                                             Query Match 73.4%; Score 47; DB 2; Length 367; Best Local Similarity 75.0%; Pred. No. 96; Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.4%; Score 47; DB 2; Length 895; 81.8%; Pred. No. 2.3e+02; Live 0; Mismatches 2; Indels
Gramene; Q6AV33; -.
Hypothetical protein.
SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;
                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                         895 AA.
                                                                                                                                                                       PRT;
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Q4NUK4;
                                                                                                        Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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ORFNames=AdehDRAFT_2813;
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Search completed: March 13, 2006, 19:14:28 Job time: 88.1059 secs

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Matches 12; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-791-495-9
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Sequence 20577, A
Sequence 30527, A
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Sequence 27111,
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                                                                                                                        March 13, 2006, 19:14:49; Search time 22.3059 Seconds (without alignments) 44.477 Million cell updates/sec
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               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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2: /cgn2_6/prodata/1/laa/6_COMB.pep:*
3: /cgr2_6/prodata/1/laa/H_COMB.pep:*
4: /cgn2_6/prodata/1/laa/H_COMB.pep:*
5: /cgr2_6/prodata/1/laa/RE_COMB.pep:*
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US-09-141-829A-9

US-09-341-829A-9

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                         Sequence:
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                                                                                                                            Run on:
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No.
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COUNTRY:
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                                                          US-09-751-798-8

Sequence 8, Application US/09751798

Sequence 8, Application US/09751798

Sequence 8, Application US/09751798

Sequence 8, Application US/09751798

APPLICANT: Stockert, Elisabeth; Jager, Elke;

APPLICANT: Stockert, Stockert, John Usyd J.

TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer;

TITLE OF INVENTION: Associated Proteins, Uses Thereof;

TITLE OF INVENTION: Binding Peptides Derived Therefrom

TITLE OF INVENTION: Binding Peptides Derived Therefrom

NUMBER OF SEQUENCES:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue

CITT: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
CAMPITER: IBM
CAMPITER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
FRIOR APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: LUD 5466.1
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEPHONE: (212) 318-3558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARASGPGGGAPR 12
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-937-263B-8
                                                          US-08-937-263B-8
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Gaps
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US-09-392-714-25

Sequence 25, Application US/09392714A

Patent No. 6686147

GENERAL INPORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Grante, Mail ameon, Barbara
APPLICANT: Chen, Yao-Teeng
FILE REFERENCE: L0461/7062
FILE REFERENCE: L0461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
FARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 30
SOOTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 180
COUNTY I 10103

ZIP 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

AMDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                      COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILLING DATE:
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HANBON, No. 6525177man D.
REGISTRATION NUMBER: 30,946
TRECESPRENCE/DOCKET NUMBER: LUD 5466,
TREECOMMUNICATION INFORMATION:
TELECPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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TOPOLOGY: linear
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Gaps
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    <151> 1998-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Chen, Iloyd J.
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: LO461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
CORRESPONDENCE: 14
CORRESPONDENCE 14
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PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 9
SEQ ID NO 9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/09849602
Patent No. 6794501
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Patent No. 5811519
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SOFTWARE: Patentin version 3.0
SEQ ID NO 30
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ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 12; Conserv
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Best Local Similarity
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                                                                                                 APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
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COMPUTER: 1BM
COMPUTER: 1BM
COMPUTER: 1BM
COPERATING SYSTEM: PC-DOS
COFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/037,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/09/126,182
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 64; DB 2; Length 180; 100.0%; Pred. No. 0.21;
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APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Palleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6723832man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6723832mai
REGISTRATION NUMBER: 30,946
                                     Sequence 15, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09341829A
Patent No. 6794131
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 180 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                    US-09-165-546D-15
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<151> 1997-01-27
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Fatent No. 6794131
GENERAL INFORMATION:
APPLICANT: Leth., Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Indee 1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPERENCE: Lo461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILLING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: BCT/US98/01445
PRIOR APPLICATION NUMBER: PCT/US98/01445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 2; Length 210;
Pred. No. 2.7;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 1; Length 210;
Pred. No. 2.7;
0; Mismatches 1; Indels
                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
    Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
IENGTH: 210
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                               L0461/7005
                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-341
                       600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 210 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5%;
91.7%;
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 91.7
Matches 11, Conservative
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51 ARASGPRGGAPR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                      USA
                                                                                 COUNTRY: U
  ADDRESSEE:
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US-09-341-829A-5
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Sequence 7, Application US/09341829A

Patent No. 6794131

GENERAL INPORMATION:
APPLICANT: Leth,, Bernard
APPLICANT: Leth, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPRENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
FRICR APPLICATION NUMBER: CT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOUTHWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 56; DB 2; Length 180; 91.7%; Pred. No. 2.3; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 180;
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; Patent No. 5811519
; GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smer, Charles
APPLICANT: Godélaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
APPLICAL...
PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Ameterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUICATION INFORMATION:
TELEPHONE: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.3, 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.5%; Score 56; Best Local Similarity 91.7%; Pred. No. 3 Matches 11; Conservative 0; Mismatch
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Best Local Similarity 91.7
Matches 11; Conservative
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LENGTH: 180
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US-08-791-495-5
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Gaps

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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARRUGINCS ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-17
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31759
LENGTH: 809
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US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Whinston, LLP
; ADDRESSEE: Whinston, LLP
; ADDRESSEE: Whinston, LLP
; ADDRESSEE: Whinston, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 2;
Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: 121 S.W. Salmon Street STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows NT SOFTWARE: WordPerfect 7.0 & ASCIICARRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/789,329C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Barp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 2847
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 01/23/97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EATP, DAVIG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                               APPLICANT: Sabin', Care...

APPLICANT: Sabin', Ugur...

APPLICANT: Ramensee, Hans Georg

APPLICANT: Ramensee, Hans Georg

APPLICANT: Ramensee, Hans Georg

APPLICANT: Ramensee, Hans Georg

TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene

TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene

TITLE OF INVENTION: Gene, and Uses Thereof

FILE REFERENCE: LUD 5556.1

CURRENT APPLICATION NUMBER: US/99/344,040C

CURRENT FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

NUMBER OF SEQ ID NOS: 132

SEQ ID NO: 117
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Fatent No. 6673350

GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Bahin, Ugur
APPLICANT: Pireundschuh, Michael
APPLICANT: Pireundschuh, Michael
TILLE REFERENCE: LUD 5622.1
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039A
CURRENT APPLICATION NUMBER: US/09/455
PRIOR APPLICATION NUMBER: US/09/344,040
PRIOR PLING DATE: 1999-06-25
PRIOR PLING DATE: 1999-06-26
PRIOR PLING DATE: 1999-06-26
PRIOR PLING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 131
SOFTWARE PLEENTIN PURSE: US/09/105,839
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100.0%; Pred. No. 4.6e+05;
tive 0; Mismatches 0;
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US-09-252-991A-31759
; Sequence 31759, Application US/09252991A
                Sequence 117, Application US/09344040C
Patent No. 6548064
GENERL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 9; Conservative
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Best Local Similarity 100...
Lag 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-09-344-040C-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RASGPGGGA 10
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US-09-344-040C-117
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Query Match
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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2 RASGPGGAPR 12 || || || || 56 RAGAPGGGGPR 66

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Db 56 RAGAPGGGGPR 66

Search completed: March 13, 2006, 19:18:52 Job time : 23.3059 secs

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial
         US-10-296-734-1404
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Sequence 30, Appl
Sequence 8, Appli
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                                                                              (without alignments)
69.096 Million cell updates/sec
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                                                                  March 13, 2006, 19:51:56; Search time 72.5647 Seconds
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                                                                                                                                                                                                                                                                                                  Published Applications AA Main: * /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: * 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: * /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-482-029-202
US-09-751-798-8
US-09-849-602-30
US-10-207-655-71
US-10-204-614-14
US-10-204-614-14
US-10-205-021-386
US-10-296-734-832
US-10-273-860-1270
US-10-877-373-9
US-10-877-373-8
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-296-734-1454
                                                                                                                                                                                  1867569 segs, 417829326 residues
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                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                          US-09-529-206E-29
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Match Length
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                                                                                                                    Perfect score:
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4, 34, App
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; Publication No. US20040054137A1
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Rambhaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor TITLE OF INVENTION: Synthetic molecules and uses therefor CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR PPLICATION NUMBER: AU PQ7761/00
; PRIOR PLICATION NUMBER: AU PQ7761/00
; ROUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; ENGTH: 30
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US-10-296-734-1436
US-10-295-027-388
US-10-188-832-141
US-10-146-473-69
US-10-117-937-75
US-10-26-734-834
US-10-65-022-75
US-10-657-022-75
US-11-067-159-75
US-11-067-159-75
US-11-067-159-75
US-11-067-159-75
US-11-067-159-75
US-11-067-159-75
US-11-067-159-76
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Sequence 202, Application US/10482029
Fublication No. US20050037445A1
GENERAL INFORMATION:
APPLICAMT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REPERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 202
LENGTH: 179
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US-10-296-734-1404
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Stockert, Elisabeth
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                                                                                                                                                                                                                                                                                                             APPLICANT: Stocker, Elisabeth, Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Attibodies Which Bind to NY-ESO-1, and HLA
TITLE OF INVENTION: Truncated Proteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STREET: New York
COUNTRY: USA
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100.0%; Score 64; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels
100.0%; Score 64; DB 5; Length 179; 100.0%; Pred. No. 0.93; ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 'Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. US20020010321Alman D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 5466.3
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                 Sequence 8, Application US/09751798
Patent No. US20020010321A1
GENERAL INFORMATION:
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Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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TOPOLOGY: linear
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Sequence 30, Application US/09849602
Publication No. US20030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.

US-09-849-602-30

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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage COMPUTER: 184
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. US20020164665Alman D. REGIGSTRATION NUBBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
STREET: New York
CITY: New York
COUNTRY: USA
APPLICANT: Chen, Yao-reeng
TITLE OF INVENTION: COLON Cancer Antigen Panel
FILE REPERBENCE: L046/1/105 (URV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIORIGATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <underwedth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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US-09-849-602-30
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Gaps
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100.0%; Pred. No. 0.94;
ive 0; Mismatches 0; Indels
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                       APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: EPITODE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFRENCE: CTLIMM.21CPIC
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT APPLICATION NUMBER: 09/561,074
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
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PUBLICATION NO. US20030220239A1

GENERAL INFORMATION:
APPLICANT: SIMARD, John, J.L.
APPLICANT: SIMARD, John, J.L.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: KIE, Zhidong
TITLE REFERENCE: CTILMM.027A
CURRENT APPLICATION NUMBER: US/10/117, 937
CURRENT PILING DATE: 2002-04-06
FRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
NUMBER: OF SEQ ID NOS: 602
SEQ ID NO 74
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Best Local Similarity 100.0.
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Matches 12; Conservative
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ORGANISM: Homo sapiens
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Sequence 14, Application US/10364614

Sequence 14, Application US/10364614

Sequence 14, Application US/10364614

Sequence 11, Application No. USC03030175250A1

SERBEAL INFORMATION:

APPLICANT: Alexander

APPLICANT: OLD, Lloyd

APPLICANT: OLD, Lloyd

APPLICANT: OLD 5126.1 CIP

FILLE REPRENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR PILLING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                      Sequence 71, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REPERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
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100.0%; Score 64; DB 4; Length 180;
100.0%; Pred. No. 0.94;
ive 0; Mismatches 0; Indels
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; Publication No. US20030215425A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match (100.
Best Local Similarity 100.
Matches 12; Conservative
                                                   12; Conservative
                                                                                                  1 ARASGPGGGAPR 12
                                                                                                                                 1 ARASGPGGGAPR 12
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US-10-207-655-71
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                            Best Local Similarity
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LENGTH: 180
TYPE: PRT
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     Query Match
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                                                   Matches
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TYPE: PRT
ORGANISM: Homo sapiens
                              TYPE: PRT
ORGANISM: Artificial
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LENGTH: 180
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                                                                                                                        APPLICANT: Atai, Natasha
APPLICANT: Atai, Natasha
APPLICANT: Atai, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Glyne, Richard
APPLICANT: Mack, David H.
APPLICANTON WORBER: US (0) 50.027
CURRENT FILING DATE: 2000-09-15
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION WUMBER: US (0) 332, 464
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-3
PRIOR FILING DATE: 2002-01-10
PRIOR PRIOR PRIOR DATE: 2002-01-10
PRIOR PRIOR DATE: 2002-01-10
PRIOR PRIOR DATE: 2002-01-10
PRIOR DATE: 2002-01-10
PRIOR 
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; Sequence 832, Application US/10296734
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR PILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SEQ ID NO 832
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                          Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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LENGTH: 180
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US-10-188-832-139

Sequence 139, Application US/10188832

Publication No. US20040076955A1

GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eas Biotechnology, Inc.

TITLE OF INVENTION: Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: And Methods of Screening for Modulators of Bladder

FILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US 60/302,814

PRIOR FILING DATE: 2001-07-03

PRIOR FILING DATE: 2001-08-03

PRIOR PELICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-11-08

PRIOR PELICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13
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Sequence 11, Application US/10777053

Sequence 11, Application No. US20040132088A1

Sequence 11, Daylication No. US20040132088A1

GENERAL INFORMATION:

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Calmond, David C.

APPLICANT: Lei, Xiang-Dong

TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

FILE REFRENCE: MANNK.022C1

CURRENT APPLICATION NUMBER: US/10/777, 053

CURRENT APPLICATION NUMBER: 10/292,413

PRIOR FILING DATE: 2004-02-10

PRIOR FILING DATE: 2002-11-07
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                                                                                                       Score 64; DB 4; Length 180;
Pred. No. 0.94;
; Mismatches 0; Indels
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; OTHER INFORMATION: NYNSOla consensus polypeptide
US-10-296-734-832
                                                                  100.0%; Scor.
v 100.0%; Pred. No. v..
                                                                          Ouery Match
Best Local Similarity 100.
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                                                                                                                                                            US-10-657-022-74

Sequence 74, Application US/10657022

Publication No. US20040180354A1

GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCES: MANNER: 0324
CURRENT PELING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: 60/409123

PRIOR APPLICATION NUMBER: 60/409123

PRIOR FILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 610
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                                                                           51 ARASGPGGGAPR 62
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74
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Best Local Similarity
Matches 12; Conserva
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Sequence 15, Application US/10751088
Publication No. US20040158044A1
GENERAL INFORMATION:
APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                        ö
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT: APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIPICATION: 530
PRIOR APPLICATION NUMBER: US/99/165,546D
FILING DATE: 02-OCT-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: April 17, 1998
APPLICATION NUMBER: US/99/165,546D
FILING DATE: O2-OCT-1998
APPLICATION NUMBER: US/99/125,182
FILING DATE: COCTOBER: 3, 1996
APPLICATION NUMBER: US/99/125,182
                                                                                                                                                                                                                                          DB 4; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Score 64; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York
CITY: New York
COUNTRY: USA
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 15 US-10-751-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
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                                                                                                                                                                                                                                                                                                                                 1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                51 ARASGPGGGAPR 62
                                                                                                                                        TYPE: PRT
CORGANISM: Homo Sapien
US-10-777-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-751-088-15
                                                                                                                  LENGTH: 180
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LENGTH: 180
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Sequence 20556, A
Sequence 20556, A
Sequence 2395, Ap
Sequence 22317, A
Sequence 2233, A
Sequence 2233, A
Sequence 2232, A
Sequence 2332, A
Sequence 2332, A
Sequence 38, Appl
Sequence 38, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 1762, Ap
Sequence 2722, Ap
Sequence 2722, Ap
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Appli
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                                                      March 13, 2006, 19:54:06; Search time 8.18824 Seconds (without alignments) 40.793 Million cell updates/sec
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Sequence 2, Ap
Sequence 54, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                           Published Applications AA New:*

1: /cgn2 6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/USI0 NEW PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/USI1 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                    161667 segs, 27834885 residues
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Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                               US-09-529-206E-29
64
                                                                                                                  1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                               Title:
Perfect score:
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40
40
                                     OM protein
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                                                                                                                                                                   Searched:
                                                                                                                    Sequence:
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No.
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26 39 60.9 618 7 US-11-078-735-18 Sequence 18, Appl 29 60.9 618 7 US-11-03-077-18 Sequence 63, Appl 29 60.9 66.9 7 US-11-03-077-18 Sequence 18, Appl 30 60.9 66.2 7 US-11-072-175-184 Sequence 18, Appl 31 32 38.5 60.9 836 7 US-11-154-227-105 Sequence 105, Appl 32 38.5 60.9 904 7 US-11-164-227-97 Sequence 105, Appl 33 38 59.4 132 7 US-11-096-568-1390 Sequence 105, Appl 35 38 59.4 162 7 US-11-096-568-14323 Sequence 14323, Appl 36 59.4 162 7 US-11-096-568-1457 Sequence 14323, Appl 38 59.4 235 7 US-11-096-568-16457 Sequence 22845, Appl 38 59.4 235 7 US-11-096-568-2604 Sequence 22845, Appl 38 59.4 236 7 US-11-096-568-2604 Sequence 22603, Appl 41 38 59.4 274 7 US-11-096-568-2603 Sequence 22603, Appl 42 38 59.4 274 7 US-11-096-568-2603 Sequence 22603, Appl 43 59.4 236 7 US-11-096-568-98 Sequence 22603, Appl 44 38 59.4 428 7 US-11-096-568-98 Sequence 1628, Appl 44 38 59.4 428 7 US-11-096-568-98 Sequence 1628, Appl 44 38 59.4 438 6 US-10-091-234-1628 Sequence 9, Appl 44 38 59.4 438 6 US-10-091-234-1897 Sequence 9, Appl 44 38 59.4 438 6 US-10-091-234-1897 Sequence 9, Appl 44 38 59.4 438 6 US-10-091-239-38
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## ALIGNMENTS

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195-11-15-288-7

Sequence 7, Application US/11155288

Publication No. USZOGGO008468A1

GENERAL INPORMITION: Chih.Sheng

APPLICANT: Simard, John J.L.

TITLE OF INVENTION: CAMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

TOWNER OF SEQ 10 NOS 1.00.40.96.959

MUMBER OF SEQ 10 NOS 1.00.40.96.97

MUMBER OF SEQ 10 NOS 1.00.08.96.969

MUMBER OF SEQ 10 NOS 1.00.08.969

MUMBER OF SEQ 10 NOS 1.00.08.969

MACCHER DEADLY TYPE: PRT

MASSOCIATE OF WINDOWS Version 4.0

MACHES OF COMBINISM: HOME SEQUENCE OF MISMATCHES 0. Indels 0. Gaps 0.9

MACHES OF COMBINATION: RECOMBINATION: REPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: RECOMBINATION: RECOMBINATION: RECOMBINATION: RECOMBINATION: REPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: MUMBER: US/11/021,441

MERCAN APPLICATION WUMBER: US 60/616,750

PRICE THE PREMERE OF TUMOR OF TILLING DATE: 2004-10-06

PRICE ARROW APPLICATION WUMBER: US 60/616,750
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Gaps

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Sequence 23806, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 150-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 23806
LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 134;
                                                                                                                                                                                                       Length 306;
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                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                     Score 47; DB 7;
Pred. No. 9.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 7;
Pred. No. 6.4;
                                                                                                                   ) LOCATION: (1)...(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , LOCATION: (1).7(134)
, OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
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APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOWU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-072-512-3295
Sequence 3.295, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                             TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays subsp. mays
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SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                         73.4%;
81.8%;
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72.7%;
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OTSUKI, TETSUJI
                                                                                                                                                                                   Query Match
Best Local Similarity 81.0.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.9
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                             91 ARADGPGTGAP 101
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NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                             1 ARASGPGGGAP 11
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                                                                   FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
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APPLICANT:
APPLICANT:
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APPLICANT:
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT A Lexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1592PUS2
CURRENT PILLING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20556
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Reanget, Marc W.
APPLICANT: Reanget, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012.1.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 496
LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 64; DB 7; Length 240; Best Local Similarity 100.0%; Pred. No. 0.04; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.2%; Score 52; DB 6; Length 20;
100.0%; Pred. No. 0.19;
tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-05
PRIOR FILING DATE: 2004-05
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR PILING DATE: 2004-03-26
PRIOR PILING DATE: 2004-03-26
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 28
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 496, Application US/10623155; Publication No. US20050261166A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Fusion protein
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ARASGPGGGAPR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 10, Conservative
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US-11-096-568A-20556
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US-10-623-155-496
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Gaps

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US-11-066-568A-22333 Application US/11096568A
Sequence 22333, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF EDG ID NOS: 34471
SEQ ID NO 22333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27265, Application US/11096568A
| Sequence 27265, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| TITLE REPRENCE: 2750-1592P025
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 27265
| LENGTH: 413
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                                                                                    Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 358
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                                                                                    Score 43; DB 7;
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
  ; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334
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CTHER INFORMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1). (358)
; OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB
Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                       67.2%;
                                                                                                                                                                                                                 109 ARGQGPGGEQPR 120
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Best Local Similarity 66...
8; Conservative
                                                                                  Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Publication No. US20060048240A1
GENERAL INFORMATION:
FULL INFORMATION:
FILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
ENGRENT 558
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Sequence 22334, Application US/1109556BA

Sequence 22334, Application US/1109556BA

Sequence 22334, Application US/10060048240A1

GENERAL INFORMATION: USOURCE at al.

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REPRENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,56BA

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22334

LENGTH: 353
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Pred. No. 35;
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Pred. No. 41;
0; Mismatches
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US-11-096-568A-26217
                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
               CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION, UMBER: UP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3295
LENGTH: 678
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80.0%;
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ilarity 66.7%;
Conservative
FILE REFERENCE: 084335-0191
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                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.0
Matches 8; Conservative
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592 RAAGPGGGWP 601
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                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-072-512-3295
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Best Local Similarity
Matches 8; Conserv
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Gaps
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Pred. No. 1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 7; Length 537;
Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                GENERAL INFORMATION:
APPLICANT: Chalfant, Charles E.
APPLICANT: Hannun, Yusef A.
APPLICANT: Bettus, Benjamin J.
APPLICANT: Bielawska, Alicja
ITILE OF INVENTION: Ceramide Kinase and Uses Thereof
FILE REPERBUS: 9175-028-999 (MUSC Ref P0401)
CURRENT APPLICATION NUMBER: US/11/179,958A
CURRENT APPLICATION NUMBER: 60/586,909
PRIOR PILING DATE: 2004-07-09
PRIOR FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Human ceramide kinase US-11-179-958A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3369, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSURI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.1%;
70.0%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
Publication No. US20060030537A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70...
Translation 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3369
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IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIO, YURI
OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RASGPGGGAP 11
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US-11-072-512-3369
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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APPLICANT:
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                                                                       Sequence 22332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22332
LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%; Score 43; DB 7; Length 420; 66.7%; Pred. No. 43; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/11108528
Publication No. US20050261189A1
GENERAL INFORMATION:
APPLICANT: Lareen, Glenn
APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Chen, C. M. Amy
APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: METHOR-POI-18
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT APPLICATION NUMBER: US 60/563,137
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR APPLICATION NUMBER: US 60/598,368
NUMBER OF SEQ ID NOS: 86
SOFTRARE FREENER PRESED for Windows Version 4.0
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| LOCATION: (1):7(420)
| TOTHER INDORMATION: Ceres Seq. ID no. 12408542
| US-11-096-568A-22332
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                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Best Local Similarity 80.0
Lac 8; Conservative
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Matches 8; Conservative
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LENGTH: 365
TYPE: PRT
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US-11-179-958A-2
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                                                                                                                         Sequence 66, Application US/11037243

| Publication No. US20050287546A1
| GENERAL INFORMATION:
| APPLICANT: CARREBELS, SEAN
| APPLICANT: CARREBELS, SEAN
| APPLICANT: CHARYDCANK, GIEN
| APPLICANT: CHARYDCANK, GIEN
| APPLICANT: CHARYDCANK, GIEN
| APPLICANT: CHARYDCANK, SUCHAN, APPLICANT: CHARYDCANK, SUCHAN, TITLE OF INVENTION: NOVEL PROTEASES
| FILE REFERENCE: 038602/1214
| CURRENT APPLICATION NUMBER: US/09/888,615
| PRIOR PILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-26
| NUMBER OF SEQ ID NOS: 150
| SOFTWARE: PATENTIN VEY: 2:1
| SEQ ID NO 66
| LENGTH: 953
| TYPE: PRT
| TYPE: PRT
| ORGANISM: HOMO SADIENB
473 ASGPGSGSP 481
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US-11-037-243-66
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Search completed: March 13, 2006, 20:03:31 Job time : 8.18824 secs

214 GPGGGHPR 221

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16-AUG-1999
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                                                                                                     March 13, 2006, 18:52:59 ; Search time 82.8235 Seconds (without alignments) 58.355 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
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60
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Maximum DB seq length: 200000000
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                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay06066 Human can	Aay06065 Human can			Aay05978 Human can	Aay05979 Human can	Aau85105 Human NYN	Adk68648 Epitope 1	Aaw62584 Cancer as	Aaw69665 Human NY-	Aay05965 Human can	Aay52430 Human tum	Aay70862 Human tum	Aab03154 Human oes	Aab69946 Human NY-	Aag67164 Amino aci	Aau01535 Human NY-	Aae07714 Human NY	Aau84818 Human NYN	Aau11543 Human tum	Abr58672 Human can	Abr48210 Human bla		Abu56694 Lung canc
SUMMARIES	a	AAY06066	AAY06065	AAY06064	AAY05986	AAY05978	AAY05979	AAU85105	ADK68648	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164	AAU01535	AAE07714	AAU84818	AAU11543	ABR58672	ABR48210	ABU56508	ABUS6694
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		Abr83438 Human NY-	Adc09576 NY-ESO-1	Add35564 Human NY-	Add35568 Human NY-	Add25510 Binding d	Adn39068 Cancer/an	Adj54139 Human NY-	Adm72815 Human NY-	Adm73418 CAG-3 pro	Adm73417 Human NY-	Adg18451 Human sof	Adq10446 Autoimmun	Ads80926 Tumour as	Adw44353 Human aut	Ady85096 Tumor ant	Adz28913 NY-ESO-1	Adz42374 Immunogen	Aea35651 Human NY-	Adw99402 NY-ESO-1/
ABP74198	ABU64816	ABR83438	ADC09576	ADD35564	ADD35568	ADD25510	ADN39068	ADJ54139	ADM72815	ADM73418	ADM73417	ADQ18451	ADQ10446	ADS80926	ADW44353	ADY85096	ADZ28913	ADZ42374	AEA35651	ADW99402
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18	180	180	180	180	18	180	180	180	18	18	18	180	18	18	18	180	18	180	180	24
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

This peptide corresponds to amino acid residues 52-62 of human NY ESO-1/CAG-3 ORFI (see AAY05955), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such ase primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-lodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; carcer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic I lymphocyte; CTL. Human cancer antigen NY ESO-1/CAG-3 peptide. (USSH ) US DEPT HEALTH & HUMAN SERVICES. Example 11; Page 50; 88pp; English. AAY06066 standard; peptide; 11 AA. Cancer antigen NY ESO1/CAG-3. 98WO-US019609 97US-0061428P (first entry) Wang RF, Rosenberg SA; WPI; 1999-277270/23. WO9918206-A2. 21-SEP-1998; Homo sapiens 08-OCT-1997; 15-APR-1999. 

(first entry)

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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; retrine cancer; breast cancer; postate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; parcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic T lymphocyte; CTL.
                                                                                                                                       Human cancer antigen NY ESO-1/CAG-3 peptide.
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                                                       AAY06064 standard; peptide; 13 AA.
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cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide corresponds to amino acid residues 51-62 of human NY ESO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
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                                                                      2; Length 11;
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                                                                    100.0%;
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                                                      Query Match
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Matches 11; Conserv
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                                          Sequence 11 AA;
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                                                                                                                                                                                                                                                   AAY06065;
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97US-0061428P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                                                                                                 Example 11; Page 50; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY05986 standard; peptide; 14 AA.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                             Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-1999 (first entry)
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Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RASGPGGGAPR
                                            WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
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RASGPGGGAPR 12

cervical

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The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their cancer rose (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonuclectides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, which no cancers such as primary or metastatic melanoma, thymoma, lung cancer, luver cancer, leukaemia, uterine cancer, lymphoma, sarcoma, lung cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; ervical cancer; bladet cancer; kidney cancer; panozeatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NY ESO-1/CAG-3 gene, CAG-3 gene, cancer peptide, antigen; human, leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 60; DB 2; Length 14; 100.0%; Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; Page 50; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                          98WO-US019609
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18 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14 AA;
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                              WO9918206-A2
                                                                                                                                                                                                                                                                          21-SEP-1998;
                                                                                                                                                                                                                                                                                                              08-OCT-1997;
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                                                                                                                      vaccine.
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The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAVO5955), a new and potent tumour antigen capable of eliciting an attigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAVO5966), portions of them and their cacc. CAG-3 ORF2 (see AAVO5966), portions of them and their cacc. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or inhibiting cancer by administering a cancer peptide, useful in diagnostic and detection assays; and methods cancer peptide or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastetic melanoma, thymoma, carvical cancer, bladder cancer, leukaemia, uterine cancer, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer and adenocarcinomas such cancer by inducing cancer, liver cancer and adenocarcinomas such cancer between the cancer peptide in vitro for subsequent
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cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; Jung cancer; metastasis; metanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; parcoma; therapy; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 60; DB 2; Length 15; 100.0%; Pred. No. 0.18;
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                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY05979 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                     Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                    98WO-US019609.
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                                                                                                                                                                                                                                                                                                                       Wang RF, Rosenberg SA;
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Best Local Similarity
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                                                                                 Homo sapiens
                                                                                                                     WO9918206-A2
                                                                                                                                                                                                                                        08-OCT-1997;
                                                                                                                                                                                                  21-SEP-1998;
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                                       vaccine.
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AAY05979
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25-MAY-2001; 2001WO-AU000622
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                                                                                                                                            Thomson SA,
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  X B X S X X X X X X X B X B X B X Y X Y X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CMG-3 (or CMG-3) ORF1 (see AAVO5965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAVO5966), portions of them and their variants (see AAVO5967-3 ORF2 (see AAVO5966), portions of them and their variants (see AAVO5967-3 ORF2 (see AAVO5966), portions of them and their variants (see AAVO5967-3 ORF2 (see AAVO5966), portions of them and their variants (see AAVO5967-3 ORF2 (see AAVO5966), portions of them and their variants of method of diagnosis of cancer or precancer; a transgenic animal; antipodies reacting with a CAG-3 cancer peptide, or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an cancer such as primary or metasteric melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancers bladder cancer, liver cancer, leukaemia, uterine cancer, cervical gracomer, bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                 98WO-US019609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NYNSOla segment 4.
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    Homo sapiens
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                                                                      WO9918206-A2
                                                                                                                                                                 21-SEP-1998;
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                                                                                                                   15-APR-1999
                            Synthetic.
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                                                                                                                                                                                                                                                                                                         Wang RF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patient
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Matches
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the invention relaters to a new syminatic polypeptide (1) comparation geveral different segments to a new symination polypeptide (1) competed to the control of a teast one parent polypeptide in the control of associated with the parent polypeptide and inducing an function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polyperide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptide sad polymorlocities are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for cancer, (e.g., cancers of the lung, brasst, ovary, cervix, colon, head and neck, panoreas, prostate, stomach, bladder, kidney, bone liver, concertions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Bar virus and respiratory syncytial virus), bacterial (e.g., infections caused by Plasmodium, Schistosma, Leishmania, Trypanosoma, Toxoplasma and Giandia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the
                                                                                                                                                                                                                                                                                                                                                                                                                  New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitope liberation; substrate; proteasome; cytostatic; antibacterial; protezoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new synthetic polypeptide (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epitope liberation-related NY-ESO-1 protein SegID11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK68648 standard; protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 27; 364pp; English
26-MAY-2000; 2000AU-00007761.
                                                                                   (AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                             WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Bite" gite"

(SIMA/) S (DIAM/) I (QIUZ/) C (LEIX/) I

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The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification describbed a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an NHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 60; DB 2; Length 180; 100.0%; Pred. No. 1.5; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gure A, Old LJ, Jager E, Knuth A;
                                                                         note= "potential myristorylation site"
                                                                                                                                                                                                                                                                /note= "potential phosphorylation site"
                             note= "potential myristorylation site"
                                                                                                                                                                                                                 'note= "potential phosphorylation site"
                                                                                                                                                                     'note= "potential phosphorylation
                                                                                                                       note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW69665 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US016335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00725182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-286417/25.
                                                                                                                                                                                         Misc-difference 134
                                                                                                                                                                                                                                       Misc-difference 138
                                                                                                                                             Misc-difference 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                               Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic regime
       Misc-difference 7
                                                   Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV38566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drijfhout JW;
                                                                                                                                                                                                                                                                                                              WO9814464-A1
                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-0CT-1998
                                                                                                                                                                                                                                                                                                                                                       09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW69665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate with a composition including the proteasome, and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, proteasome of compounds with a cytostatic, antibacterial, proteasome of compounds with a cytostatic, antibacterial, contaction may allow development of a vaccine. The invention is useful for identified housekeeping epitope. The compositions comprising where the epitope is a housekeeping epitope. The compositions comprising contaction for identified housekeeping epitopes are useful in vitro in vaccine development or in the generation or expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunotherapy. The invention is also useful con the knowledge that such epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the contemporation processome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing target cells in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                      Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 60; DB 8; Length 179; 100.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                           Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 11; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW62584 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                           Qiu Z,
                                           07-NOV-2002; 2002US-00292413.
                                                                                          07-NOV-2001; 2001US-0336968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1998 (first entry)
                                                                                                                                                                                                                                                           Simard JJL, Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                              ) DIAMOND D C. ) QIU Z. ) LEI X.
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                                                                                                                                                                                                                                                                                                       2004-167209/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                             N-PSDB; ADK68674
11-DEC-2003
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Gaps

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Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

Ношо варіепв WO9832855-A1

Location/Qualifiers

Ното варіеля

Key

AAW62584;

RESULT 9

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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and content tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965. CC AAY05966), portions of these peptides and their variants (see AAY05965. CC AAY05966), portions of these peptides and their variants (see AAY05965. CC AAY05966), portions of these peptides that inhibit eroperasion of the cancer peptide, useful in diagnostic and detection assays; and methods CC ancer peptide, useful in diagnostic and detection assays; and methods of the cancer peptide, useful in diagnostic and detection assays; and methods correspond or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, corroral cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is transed by inducing cancer specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60. .68
/note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Peptide presented by MHC Class I HLA-B7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 60; DB 2; Length 180; 100.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY52430 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                           Cancer antigen NY ESO1/CAG-3.
                                                                          97US-0061428P
                          98WO-US019609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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/note= "
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                                                                                                                                                                           Wang RF, Rosenberg SA;
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                                                                                                                                                                                                                                WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                return to a patient
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                                                                                                                                                                                                                                                           N-PSDB; AAX58599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180 AA;
                          21-SEP-1998;
                                                                        08-OCT-1997;
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Unidentified.
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15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment and all AFA presenting contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; carcier; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; tumour; diagnosis; immunotherapy; therapy; vaccine; ORFI.
                                                                                                                                                                                                                                                                                                                                   New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders,
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                                                                                                                                                                                                        Godelaine D, Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 60; DB 2; Length 180; 100.0%; Pred. No. 1.5; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 57-58; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY05965 standard; protein; 180 AA.
                                                                                                                                                                                                        De Smet C,
                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                  98WO-US001445
                                                                                                   97US-00791495
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                                                                                                                                                                                                                                                                                                                                                                                         particularly tumours.
                                                                                                                                                                                                                                                           WPI; 1998-427951/36.
                                                                                                                                                                                                        Lucas S,
                                                                                                                                                                                                                                                                                   N-PSDB; AAV50348.
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30-JUL-1998
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/note= "Peptide presented by MHC Class I HLA-A24 and HLA-
                                                                                                                                                                                                                                       113. .122
/note= "Peptide presented by MHC Class I HLA-B5 and HLA-B52"
B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-
                                                                                                       84. 92
/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
                                       by MHC Class I HLA-B7, HLA-B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               156. .167
/note= "Peptide (AAY52434) presented by MHC Class
                                                                                      .91
re= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                             88. .96
/note= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                 /note= "Peptide presented by MHC Class I HLA-B44"
107. .116
                                                                                                                                                                                      /note= "Peptide presented by MHC Class I HLA-B44"
102. .110
                                                                                                                                                                                                              107. .116
/note= "Peptide presented by MHC Class I HLA-A24"
                                                                                                                                                                                                                                                                                                                                        note= "Peptide presented by MHC Class I HLA-A24"
138. 147
                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Peptide presented by MHC Class I HLA-B52"
[54. .163
                                                                                                                                                                                                                                      'note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                      113. .121

//note= "Peptide presented by MHC Class I HLA-B7"

115. .124

//note= "Peptide presented by MHC Class I HLA-A3"

118. .126
                                                                                                                                                                                                                                                                                                                'note= "Peptide presented by MHC Class I HLA-B35"
                                                                                                                                                                                                                                                                                                                              note= "Peptide presented by MHC Class I HLA-B52"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Peptide presented by MHC Class I HLA-B52"
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/note= "Peptide presented by MHC Class I HLA-B52"
                       presented by MHC Class I HLA-B7"
                                                                               presented by MHC Class I HLA-Al"
                                                                                                                                       "Peptide presented by MHC Class I HLA-Al"
                                                                                                                                                                     /note= "Peptide presented by MHC Class I HLA-B7"
100. .108
                                                                                                                                                                                                                                                                                                                                                               'note= "Peptide presented by MHC Class I HLA-B8"
                                                                                                                                                                                                                                                                                                                                                                      139. 147
'note= "Peptide presented by WHC Class I HLA-B7"
       "Peptide presented by MHC Class I HLA-B7"
                                                               "Peptide presented by MHC Class I HLA-A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Peptide presented by MHC Class I HLA-A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Peptide presented by MHC Class I HLA-A3"
                                        presented
                                       :e= "Peptide
HLA-B35"
                       "Peptide
                                                                               "Peptide
                                                                                                                       and HLA-B35"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                .162
                                                                                                                                                                                                                               110, 118
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               88.
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                                .87
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This sequence represents a human turmour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain turmours and turmour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other turmour types being sporadic. Peptides derived from NY-ESO-1 are bound by both MRC (major histocompastibility complex) Class I and Class II molecules for presentation to T-cells. Peptides AAV52431- Y52444 bind to Class I HLA-A2 molecules, thereby stimulating to Class II HLA-DES3 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, proliferation of T cells stimulate the proliferation of T cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                      Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                    old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                        Scanlan M, Alexander K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEIM INT GMBH. (UYHO-) UNIV HOSPITAL LEIDEN.
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                                                                    Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 30; Fig 3; 49pp; English.
(LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                               WPI; 2000-038483/03
                                                                    Stockert E, Jager
Gure A, Ritter G;
                                                                                                                                                                                                                 N-PSDB; AAZ38380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200023584-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000,
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Sahin U, Pfreundschuh M;

us-09-529-206e-30.rag

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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a CDNA library prepared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagea. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, eseveral N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The artigen is useful as an immunogen when combined with an adjuvant, in both precursor and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to besophageal cancer cells. It
                                                                                                                                                                                                                                                                                        New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can also be used to generate diagnostic or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 60; DB 3; Length 180; 100.0%; Pred. No. 1.5; ive 0; Mismatches 0; Indels
                                                                                                                                                          Chen Y, Tureci O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69946 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 3; 9pp; English.
                                                                                        (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES.
                   96US-00725381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUL-2000; 2000WO-US019220.
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                                                                                                                                                                                                                                                                                                                                          e.g. infections and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RASGPGGGAPR
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                                                                                                                                                        Gure AO,
                                                                                                                                                                                                                             WPI; 2000-410880/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180 AA;
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                     03-OCT-1996;
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                                                                                                                                                          Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB69946;
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                                                                                                                                                                                  old LJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                         The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading frame (ORF)-1 that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma) protein, a tumour-asociated antigen. The tumour-associated antigen of displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
                                                                                                                                Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnóstic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 60; DB 3; Length 180; 100.0%; Pred. No. 1.5; o; Mismatches 0; Indels
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152. .172
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Potential N-myristoylation site"
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                   Klade C;
                   Heider K,
                                                                                                                                                                                                     Example 3; Page;62-63; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB03154 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00013150
                   Aarnoudse CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-339685/29
                                                                                     N-PSDB; AAD00152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion proteins
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                   Schrier PI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6069233-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Gaps

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(CORR ) CORNELL RES FOUND INC. Jager E, Stockert E, WPI; 2001-182822/18.

N-PSDB; AAF58634.

old LJ,

Knuth A, Chen Y, Scanlan M;

Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NW-ESO-1 specific antibodies in a sample taken from a

Example 5; Fig 3; 50pp; English.

The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for emeaining whether a cancerous condition is progressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder 

Sequence 180 AA;

Gaps . 0 100.0%; Score 60; DB 4; Length 180; 100.0%; Pred. No. 1.5; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 11; Conservative Query Match

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1 RASGPGGGAPR 11 

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Search completed: March 13, 2006, 19:04:00 Job time : 83.8235 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 13, 2006, 19:04:24 ; Search time 13.0706 Seconds (without alignments) 80.975 Million cell updates/sec

US-09-529-206E-30 60 1 RASGPGGGAPR 11 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Liscing first 45 summaries

PIR 80:* Database :

1: pirl:* 2: pir2:* 3: pir2:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		do				
Result No.	Score	Query Match	Length	DB	ID	Description
1	44	73.3	3190	5	T13828	CREB-binding prote
7	42	70.0		7	S50754	
е	42	70.0		7	C87425	Ε
4	41	68.3	173	~	AB3648	flagellar basal-bo
ស	41	68.3	286	7	S04673	H+-transporting tw
9	41	68.3		~	F82878	XAA-PRO aminopepti
7	41	68.3		~	T00378	KIAA0641 protein -
æ	40	66.7	335	~	S08341	myristylated alani
6	40	66.7		7	T39312	
10	40	66.7		7	A86182	
11	40	66.7		~	T36104	Ω
12	40	66.7		~	A29345	steroid hormone re
13	40	66.7	619	~	S02165	requlatory protein
14	40	66.7		N	A87431	
15	39	65.0		~	C72683	hypothetical prote
16	39	65.0		7	B45036	Pur beta - human (
17	39	65.0		~	E87464	competence/damage-
18	39	65.0		N	900691	histocompatibility
19	39	65.0		~	T35619	hypothetical prote
20	39	65.0		7	F95899	
21	39	65.0	307	7	B72677	hypothetical prote
22	39	65.0		7	T52451	endopeptidase Clp
23	39	65.0		~	F95307	conserved hypothet
24	39	65.0		7	G75580	conserved hypothet
25	39	65.0		7	T34842	probable transfera
26	39	65.0	575	7	835327	protein kinase sqq
27	39	65.0		7	T30765	hypothetical prote
28	39	65.0	627	7	T35608	polyketide hydroxy
59	39	65.0	733	~	S10932	probable protein k

transducin-like en (1->4)-alpha-D-glu hypothetical prote	DNA-binding protei protein kinase sgg ovo protein - frul	calo protein - fru hypothetical prote hypothetical prote Pex-related protein	peptidyl-tRNA hydr peptidyl-tRNA hydr anther-specific pr	hypothetical prote Hypothetical Prote
C56695 JC7726 S07132	A56038 S35423 S16356 T01748	T13719 C72637 C87270 C75445	H87399 AH3506 S12246	T36874 AE3136
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743 757 886	1028 1067 1213	4116 104 112	143 145 161	185
65.0 65.0 65.0	68.00	0.000	63.3.3	63.3
9 9 9 9 9 9			3888	38
30 31 32	333	38 38 40	. 4 4 4 5 1 2 5 6	44 45

## ALIGNMENTS

RESULT 1 T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text change 09-Jul-2004
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G
Nature 386, 735-738, 1997
A; Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Reference number: Z17785; MUID:97263578; PMID:9109493

A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; P
C;Genetics:

A;Cross-references: FlyBase:FBgn0015624 A;Map position: X F;1723-1780/Domain: bromodomain homology <BRO>

Gaps ö Query Match 73.3%; Score 44; DB 2; Length 3190; Best Local Similarity 77.8%; Pred. No. 2.3e+02; Matches 7; Conservative 1; Mismatches 1; Indels

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:||||| || 320 NGPGGGGPR 328 3 SGPGGGAPR 11 δ 셤

hypotherical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: L4-Uul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754
A;Accession: S50754
A;Accession: S50754
A;Accession: S50754
A;Accession: Dreliminary
A;Accession: J251-4WOE>
A;Accession: J251-4WOE>
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PI

ö Query Match 70.0%; Score 42; DB 2; Length 351; Best Local Similarity 80.0%; Pred. No. 69; Matches 8; Conservative 0; Mismatches 2; Indels

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Gaps

1 RASGPGGGAP 10 g ઠે

299 RASPPGGGPP 308

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A;Status: not compared with conceptual translation A;Molecule type: DNA
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757 ATGPSGGQPR 766
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: F82878
A; Status: preliminary
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                                                                                               addose 1-epimerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87425
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87425
A;Accession: C87425
A;Molecule type: DNA
A;Residues: 1-378 cSTO>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; F
C;Genetics:
A;Gene: CC1418
C;Superfamily: aldose 1-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession. AB3648
C;Accession. AB3648
R;DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-173 <KKTS>
A;Residues: 1-173 <KKTS>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI000058740; GB:AE008918; PIDN:AAL54349.1;
A;Experimental source: strain 16M
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H+-transporting two-sector ATPase (BC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
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R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Titler: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription. A;Reference number: S04666; MUID:85058188; PMID:6209404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
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53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No.
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A, Status: preliminary
A, Molecule type: DNA,
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A; Map position: II
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                                                      RESULT 3
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XAA-PRO aminopeptidase UU532 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: F83878 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mix A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Jul-2000
C;Date: 01.Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00378
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N
DNA, Res. 5, 16-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A;Reference number: Z14142; MUID:9940380; PMID:974811
A;Accession: T00378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA *
Kresidues: 1-357 cGLA-
A;Cross-references: UNIPARC:UP100000CLCAC; GB:AE002152; GB:AF222894; NID:G6899532; PIDN
A;Experimental source: serovar 3; biovar 1
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A,Molecule type: DNA
A,Residues: 1-286 <TYB>,
A,Cross-references: UNIPROT:P05436, UNIPARC:UPI0000126582
C,Superfamily: H(+)-transporting ATP synthase gamma chain
C,Superfamily: H(+) biosynthesis; hydrolase; membrane-associated complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 357;
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A,Molecule type: mRNA
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                                                                                                                                                                                Score 41; DB 2;
Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.3%; Score 41; DB 77.8%; Pred. No. 97; tive 1; Mismatches
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A;Genetic code: SGC3
C;Superfamily: X-Pro aminopeptidase
                                                                                                                                                                                      68.3%;
80.0%;
                                                                                                                                                                                   Query Match 68.3
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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A;Residues: 1-371 <WOO>
A;Cross-references: UNIPROT:O42905; UNIPARC:UPI00011352D5; EMBL:AL022117; PIDN:CAA17929
A;Experimental source: strain 972h-; cosmid c119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dypothetical protein [imported] - Arabidopeis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: As C.S. As C
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A;Cross-references: UNIPROT:Q9MAT5; UNIPARC:UPI00000A6788; GB:AE005172; NID:g7211979; P
C;Genetics:
                                        C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39319 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
B;Wood, V; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Bubmitted to the EMBL Data Library, March 1998
A;Reference number: 221843
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hypothetical protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                 A;Accession: T39312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Introns: 77/3; 105/3; 165/3; 250/1; 276/2
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Matches 7; Conservative
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A;Molecule type: DNA
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Best Local S:
Matches 7
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                                                                 myristylated alanine-rich protein kinase C substrate - bovine
NyAlternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C;Species Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; $29270; A46098; PS0338
S;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinase
A;Reference number: S08341; MUID:89282412; PMID:2734111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown
A;Ratus: nucleic acid sequence not shown
A;Racidues: 1-98, 02, 10-0335 <ST2>
A;Residues: 1-98, 02, 10-0335 <ST2>
A;Cross-references: UNIPARC:UP1000017750A; GB:M24638; GB:M23738
A;Cross-references: UNIPARC:UP1000017750A; GB:M24638; GB:M23738
B;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protein carequivalent genes in different species.
A;Reference number: S29267; MUID:93011168; PMID:1396720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P12624; UNIPARC:UP1000016C340; EMBL:M24638; NID:g163339; PIC R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J. Proc. Netl. Acad. Sci. US.A. 86, 4012-4016, 1989 A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-A;Reference number: A32904; MUID:89264553; PMID:2726763
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A;Residues: 2-11 <MAN>
A;Residues: 2-11 <MAN>
A;Creschues: 2-11 <MAN>
A;Creschues: 2-11 <MAN>
B;Mizuteni, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
A;Reference number: PS0338; MUID:92171958; PMID:1540183
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A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
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C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 191-233, SBE', 257-279, 283-292, 'V', 294,' PEQE', 299,'A', 300,'A', 302-313,'A', 315
A; Residues: 191-233, SBE', 257-279, 283-292,'V', 294,' PEQE', 299,'A', 300,'A', 302-313,'A', 315
A; Cross-references: UNIPARC: UPI000017750B
R; Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
A; Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
A; Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
A; Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A; Accession: A46098; MUID: 93216617; PMID: 8463217
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A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
A;Cross-references: UNIPARC:UP1000017750D; UNIPARC:UP1000017750E; UNIPARC:UP1000017750F;
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A; Residues: 1-335 <STU>
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Best Local Similarity
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C;Genetics:
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36104
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36104

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Gaps

4

288 AAGPGCPRAGGAPR 301

RESULT T39312

2 ASGPG----GGAPR 11 9; Conservative

> ò g

Matches

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

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77.8%; Pred. No. 2.3e+02; ative 0; Mismatches 2;
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77.8%;
                          7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                              2 ASGPGGGAP 10
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-103 <KAW>
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A;Molecule type: DNA
A;Residues: 1-954 <STO>
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Ridguere, V.; Yang, N.; Segui, P.; Evans, R.M.

Rature 31, 91-94, 1988

A; Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.

Rature 31, 91-94, 1988

A; Ridguere, V.; Yang, N.; Segui, P.; Evans, R.M.

Ridguere, V.; Yang, N.; Segui, P.; Evans, R.M.

A; Reference number: A29345; MUID:88122546; PMID:3267207

A; Residues: 1-521 «GIG>

A; Residues: 1-521 «GIG>

A; Residues: 1-521 «GIG>

A; Rasidues: 1-521 «GIG>

A; Residues: 1-521 «GIG>

A; Cross-references: UNIPARC:UPI000017A1DF

C; Reywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; 2; 7; 174-434 (Domain: exh transforming protein homology «ERBA>

F; 176-196/Region: zinc finger
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C;Species Caulobacter crescentus
C;Species Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
R;Kaplan, JB.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
B;Mol. Biol. 205, 71-83, 1989
A;Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A;Reference number: S02165
A;Accession: S02165
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-679 < KAP>
A;Coss-references: UNIPROT:PIS345; UNIPARC:UPI000017A8F7
C;Genetics:
A;Residues: 1-436 <MUR>
A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOED8:SCE15.01
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C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative 1
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Best Local Similarity 77.8%;
Matches 7; Conservative
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465 AGPGGGAER 473
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C,Accession: A89431
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Fitle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P15345; UNIPARC: UP1000012A8ED; GB: AE005673; NID: 913422833; F
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropys. A;Reference number: A72450; MUID:99310339; PMID:10382966
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72683
                                                                                                                                                                                                                                                                                                                                  C,Species: Caulobacter crescentus
C,Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
Gaps
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Pred. No. 3.1e+02;
0; Mismatches 2; Indels
Indels
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Pred. No. 66;
1; Mismatches
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homo sapien homo sapien homo sapien

homo sapien oryza sativ

chromobacte oryza sativ homo sapien

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OM protein

Run on:

Sequence:

Searched:

Database

Result No.

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anopheles g
azoarcus sp
anaeromyxob
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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15-DEC-1998 (Rel. 37, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen IB (Autoimmunogenic cancer/testis antigen NY
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                                          Q6av33
Q8n6h2
Q5squ1
Q6ivq3
Q6ivq3
Q7mwi2
Q7mwi2
Q7q0a9
Q5gqt4
Q7q0a9
Q5qqq4
      Q4nac6
Q96s27
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
NON_TER
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Last annotation update)
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04NAC6 9MICC
096S27 HUMAN
06AV33 ORYSA
08N6H2 HUMAN
081V03 HUMAN
06ERQ1 ORYSA
07NW12 CHRVO
08L680 ORYSA
05CQ14 HUMAN
05EQ14 HUMAN
05CQ14 HUMAN
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequenc
01-CCT-2002 (TrEMBLrel. 22, Last annotat
Hypothetical protein LAGE-2 (Fragment).
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Bust Local Similarity 100.v.
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    NCBI_TaxID=9606;
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Submitted (JUL-2001)
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Submitted (MAR-2003)
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NUCLEOTIDE SEQUENCE
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
-!- SIMILARITY: Belongs to the CTAG family.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis antigen 1-A).
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MEDLINB=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
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1. Similarity 100.0%; Pred. No. 0.49;
11; Conservative 0; Mismatches 0: Indele
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Gly-rich.
; B122C5C2C8BE1569 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
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EMBL, AJ003149; CARA05908.1; -; mRNA.
EMBL, AF038567; AAD05202.1; -; mRNA.
HGNC; HGNC:2491; CTAG1B.
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17992 MW;
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TRANSMEM 156 172
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Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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"Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
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ABTRINE-99325550; PubMed=10399963;
Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
"Interfeukin-2-induced, melanoma-apecific T cells recognize CAMEL,
unexpected translation product of LAGE-1.";
Int. J. Cancer 82:442-448(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAG2 HUMAN STANDARD; PRT; 210 AA.
O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 47, Last annotation update)
Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [7]
NUCLECTIDE SEQUENCE.
Lethe B.G.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
EMBL; AJ275577; CAB76943.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
CROUENCE 180 AA; 17992 MW; B122C5CZCGBE1569 CRC64;
                                                                                                                                                                            Platzer M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 60; DB 2; 100.0%; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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us-09-529-206e-30.rup

1 RASGPGGGAPR 11

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MEDLINE-22388557; PubMed-12477932; DOI=10.1073/pnas.242603899;
WA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
WA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marunaina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marunaina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marunaina K., Farmer A.A., Rubin G.M., Hong L.,
Bacpaleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.A., McEwan P.J., McKernan K.J., Marek J.B., Garzia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garzia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rutterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQRPGTPGPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt Poly-Pro.}\\ {\tt MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPXHKV}\\
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=LAGE-1B; Synonyms=LAGE-1L;
Name=LAGE-1B; Synonyms=LAGE-1L;
ISOIG=O75638-1; Sequence=Displayed;
Name=LAGE-1A; Synonyms=LAGE-1S;
Name=LAGE-1A; Synonyms=LAGE-1S;
ISOIG=O75638-2; Sequence=VSP_004301;
ISOIG=CO75638-2; Sequence=VSP_004301;
TISSUE SPECIFICITY: Thesis and very low level in placenta and in some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; Antigen; Polymorphism; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP_004301.
R -> Q.
/FTId=VAR_007855.
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/FTId=VAR_007856.
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/FTId=VAR_007857
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EMBL, AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL, AJ223040; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ensembl; ENSG0000126890; Homo sapiens.
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AJ012835; CAA10196.1;
BC002833; AAH02833.1;
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188
210
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Complete Street 
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Burkholderiaceae, Burkholderia, pseudomallei group.
NCBI TaxID=28450;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerses III, delta subunit (EC 2.7.7.7).

Name=holA; OrderedLocusNames=BMA2451;
Burkholderia mallei (Pseudomonas mallei).

Bacferia; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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PubMed=15377793; DOI=10.1073/pna8.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                             Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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81.8%;
                                                                                                                                                                                      Q63QT8 BURPS PRELIMINARY;
Q63QT8;
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 BURMA
QE2H22 BURMA PRELIMINARY;
Q62H22;
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    RASGPRGGAPR 62
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Best Local Similarity
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SEQUENCE 362 AA;
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        52
                                                                                                                                                                 BURPS
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062H22

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DB 1, Length 210; 1; Indels

Score 52; DB 1 Pred. No. 8.3;

86.7%;

0; Mismatches

10; Conservative

Query Match Best Local Similarity Matches 10; Conserv

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13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                         Q4NUK4 9DELT PRELIMINARY;
Q4NUK4;
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          157 RAKGGGGGAPR 167
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es 9; Conserv
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Peldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugharty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.,
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
1-FBE-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein OJ191_A10.131 (Hypothetical protein
OJ1014 E06.5).
Name=OJ191_A10.131; Synonyms=OJ1014 E06.5;
Oryza sativa (sponica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae;
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0
                                                                                                                                                                                                         GO; GO:0003897; F:DNA-directed DNA polymerase activity; IEA. GO; GO:00016740; F:transferase activity; IEA. GO; GO:0005260; P:transferase activity; IEA. InterPro; IPR010372; DNA pol3 delta. InterPro; IPR005799; DNA pol3 delta. Pfem; PF044; DNA pol3 delta. TIGR044; DNA pol3 delta. TIGR0589; DNA pol3 delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.3%; Score 47; DB 2; Length 449; ilarity 81.8%; Pred. No. 94; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%; Score 50; DB 2; Length 362; 81.8%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; OFFES; -. Go. 20000151; C:ubiquitin ligase complex; IEA. GO; GO:0000151; C:ubiquitin ligase complex; IEA. GO; GO:00046872; F:metal lon binding; IEA. GO; GO:0008442; F:ubiquitin-protein ligase activity; IEA. GO; GO:0008270; F:zinc lon binding; IEA. GO; GO:0016567; F:protein ubiquitination; IEA. InterPro; IPR0008700; NOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-! SHMLARITY: Contains 1 RING-type zinc finger.
EMBL; AP003885; BAD08744.1; -; Genomic DNA.
EMBL; AP003888; BAD11573.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00184, RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
HYPOCHETical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 449 AA; 47196 MW; B8EFF7708B292296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05627; NOI; 1.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7F1E3_ORYSA PRÉLIMINARY;
Q7F1E3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 RAAGPGGDAPR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RASGPGGGAPR 11
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                          BMA2451;
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                                                                                                                                                                                          IIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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a

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RASGPGGGAPR 11

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NUCLECTIDE SEQUENCE [GENOMIC DNA / MENA].
MEDLINE=97174314; PubMed=9022048;
MCRORY J.E., Parker R.L., Sherwood N.M.;
"Expression and alternative processing of a chicken gene encoding both growth hormone-releasing hormone and pituitary adenylate cyclase-activating polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GHRH);
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PACA_CHICK STANDARD; PRT; 175 AA.
014534; Q53WW0;
01-NOV-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
11-JUL-1998 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-201 (GHP) (GRP) (Growth hormone-releasing hormone) (GHP)
13-SEP-201 (GHP) (GRP) (GRP) (GRP) (GHP)
14-SEP-201 (GHP) (GRP) (GRP) (GHP)
15-SEP-201 (GHP) (GHP) (GHP)
16-SEP-201 (GHP) (GHP) (GHP)
16-SEP-201 (GHP) (GHP) (GHP) (GHP)
16-SEP-201 (GHP) (GHP) (GHP) (GHP) (GHP)
16-SEP-201 (GHP) 
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larimer F., Land M.; "Annotation of Anaeromyxobacter" Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 895;
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81.8%; Pred. No. 1.8e+02;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
EMBL; AAHD01000013; EAL79351.1; -; Genomic DNA.
SEQUENCE 895 AA; 93871 MW; 0AE25BBBF172BDB0 CRC64;
                                                                                                                                                                                                             Last sequence update)
Last annotation update)
895 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-ORNL);
                                                                                                                                         Created)
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Name=PLEKHG2;
Homo sapiens (Human).
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                                                                                                                          NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=28450;
                                                                                         NCBI_TaxID=9606;
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Best Local S
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   셤
                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide-38.
Pituitary adenylate cyclase activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth hormone-releasing factor 1-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leucine amide (G-158 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 group).
Lysine amide (G-169 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             group).
RHADGIFSKAYRKLLGQLSARNYLHSLMAKRVG
(in isoform GRF 33-46).
/FIId=VSP_001759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PROUZIS; CLUCACON; 2.
PROSITE; PSO1260; GLUCACON; 2.
Alternative splicing; Amidation; Cleavage on pair of basic relationative splicing; Amidation; Cleavage on pair of basic relationative splicing; Glucagon family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (In isoform GRF 1-43). /FTId=VSP 001760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 1; Length 175; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODB54995FOAA9DFB CRC64;
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                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
Name=GRF 1-46;
IsoId=P41534-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                   18oId=P41534-3; Sequence=VSP 001759;
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide-27
                                                                                                                                                                                                                                                                IsoId=P41534-2; Sequence=VSP_001760; Name=GRF 33-46;
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EMBL; U71184; AAB51201.1; -; mRNA.
EMBL; U71185; AAB51202.1; -; mRNA.
EMBL; U67275; AAC64494.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
Cell Biol. 16:95-102(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000532; Glucagon.
Pfam; PF00123; Hormone 2; 2.
PRINTS; PR00275; GLUCAGON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AA; 19561 MW;
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                             PROTEIN SEQUENCE OF 131-168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Very Match
Bust Local Similarity 72.7°,
Bust Local Similarity 72.7°,
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128
168
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                                                                                                                                                                                                                                               Name=GRF 1-43;
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83
131
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TISSUB-Pancreas;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSDERG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RIJABORINE R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raheto J., Helton E., Ketteman M., Madan A., Rouffard G.G.,

Making M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roberzation and initial analysis of more than 15,000 full-length human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Kaith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
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Pred. No. 58;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Pancreas;
Director MGC Project;
Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015174; AAH15174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q63HT9_BURPS PRELIMINARY;
Q63HT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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Chromosome undetermined SCAF5395, whole genome shotgun sequence
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PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Nierman W.C., DeShazer D.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madhpu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.,
"Structural flexibility in the Burkholderia mallei genome.",
Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitchead S., Yaats C., Barrell B.G., Oyston P.C.F., Parkhill J.; Widenomic plasticity of the causative agent of melioidosis, Burkholderia pseudomalethe."; Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004). EMBL; BSZ71966; CAH39817.1; -; Genomic_DNA.
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Burkholderiaceae; Burkholderia.
                                                                                                                                                 76.7%; Score 46; DB 2; Length 327; 88.9%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.7%; Score 46; DB 2; Length 330; 88.9%; Pred. No. 97; ive 0; Mismatches 1; Indels
                                                                                                                                                                        1; Indels
                                                                                                               Complete proteome; Lipoprotein.
SEQUENCE 327 AA; 33687 MW; AC5D2C7CC4A44A25 CRC64;
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SEQUENCE 330 AA; 33977 MW; 2F12165CD7366835 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative lipoproficin.
OrderedLocusNames=BMAA2092;
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Last annotation update)
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                                                                                                                                                                                                                                                                            330 AA
                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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InterPro, IPR007428, VacJ.
Pfam, PF04333, VacJ, 1.
                                                                                         Pfam; PF04333; VacJ; 1.
PRINTS; PR01805; VACJLIPOPROT.
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                                                                                                                                                           88.9%;
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                                                                                                                                                                                                                                                                            Q629N3 BURMA PRELIMINARY;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                    243 AGGPGGGAP 251
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Best Local Similarity
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13-SEP-2005
13-SEP-2005
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Q4TEG9_TET
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Datslya C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier D., Coutanceau J.P., Gouzy J.,
Rallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptococcus neoformans var. neoformans JEC21.
Bukaryota, Fungi, Basidiomycota, Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae, Tremellales; Tremellaceae; Filobasidiella.
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PubMed=115653466; DOI=10.1126/science.1103773;
Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
                                     Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metyrydii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
Van Aken S., Fraser C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which is
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Actin Cross-linking, putative.
ORFNames=CNC06000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAE01005395; CAF88713.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the early vertebrate proto-karyotype.";
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ORFNames=GSTENG00002257001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 431:946-957(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 RPQGPGGGAP 177
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Matches 8; Conserv
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Fung E., Hyman R. W., Rowley D., Bruno D., Miranda M., Fukushima M., Wickes B.L., Fu J., Davis R.W.;

Cryptococcus neoformans serotype D sequencing.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AAEYO1000013; EAL21978.1; -; Genomic DNA.

REMBL, AAEYO1000013; EAL21978.1; -; Genomic DNA.

REMBL, AAEYO100013; EAL21978.1; -; Genomic DNA.

REMBL, CAUTION: SEAL21978.1; -; Genomic DNA.

REMBL, SAEYO100013; EAL21978.1; -; Genomic DNA.

REMBL, SAEYO100013; EAL21978.1; -; Genomic DNA.

REMBL, SAEYO1115; Calpoin actin bd.

InterPro; IPR001015; Calpoin actin bd.

InterPro; IPR001015; Spectrin.

Remain PR00107; Spectrin.

Remain PR00107; CH; 2.

RAMART; SM00033; CH; 2.

ROSITE; PS00019; ACTININ 1; UNKNOWN 1.

RROSITE; PS0001; CH; 2.

ROSITE; PS0001; CH; 2.

RHYDOLHetical protein.

SEQUENCE 708 AA; 79873 MW; BAF52DIDD2C99B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptococcus neoformans var. neoformans B-3501A.
Eukaryota; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.K., Salaberg S.L., Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Wye N.H., Kronstad J.W., Lodge J.K., Mickes B.L., Wortman J.R., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., "The genome of the basidomycetous yeast and human pathogen Cryptococcus neoformans.";
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Last sequence update)
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                                                                                                                                                                                                                                                                                       Science 307.1321-1334(2005).

EMBL; AE01343; AAW42672.1; -; Genomic_DNA.

GO; GO:0003779; F:calcium ion binding; IEA.

InterPro; IPR001999; Actnin actin bd.

InterPro; IPR001199; Actnin actin bd.

InterPro; IPR001715; Calponin act_bd.

InterPro; IPR0010192; EF-Hand type.

InterPro; IPR02017; Spectrin.

Pfam; PF00307; CH; 2.
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PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS50021; CH; 2.
COMDISCE POTCEOME.
SEQUENCE 708 AA; 79873 MW; BAFS2DID
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Matches
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Search completed: March 13, 2006, 19:14:29 Job time : 80.8471 secs

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52 RASGPGGGAPR
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Sequence 8, Appli
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Sequence 21, Appl
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                                                                                                                                                       March 13, 2006, 19:14:49; Search time 20.4471 Seconds (without alignments) 44.477 Million cell updates/sec
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                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Sequence 19986, A Sequence 562, Appl Sequence 6, Appli Sequence 30219, A Sequence 3369, A Sequence 17549, A Sequence 27111, A Sequence 115, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 19543, A Sequence 11, Appl Sequence 20189, A Sequence 11, Appl Sequence 1243, A Sequence 20189, A Sequence 201
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ZIP: 02210
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIPICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: VAN AMSTECTAM, JOHN R.
REGISTRATION NUMBER: 40,212
REGISTRATION NUMBER: 40,212
REDERMICATION INFORMATION:
TELEPOMOMICATION INFORMATION:
TELEPOMOMICATION INFORMATION:
TELEPOMOMICATION INFORMATION:
TELEPAS: 617-720-3500
TELEPAS: 617-720-2441
                          US-09-252-991A-19986
US-09-949-002-562
US-08-949-002-562
US-08-272-796-6
US-09-272-796-6
US-09-272-791A-30219
US-09-270-767-4376
US-09-252-991A-17549
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US-09-252-91A-30489
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APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 180 amino acids
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Matches 11; Conservative
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COUNTRY:
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                                                                                     Sequence 8, Application US/08937263B

Sequence 8, Application InfoRMATION:

APPLICANT: Cher, Yao-Tseng; Scanlan, Matthew;

APPLICANT: Gler, Ani; Old, Lloyd J.; Jager, Elke;

APPLICANT: Alexander, Knuth; Drijfhout, Jan W.

TITLE OF INVENTION: INSOLATED NOLECULE

TITLE OF INVENTION: INSELF, AND USES THEREOF

ITLE OF INVENTION: ITSELF, AND USES THEREOF

CORRESPONDENCES:

ADDRESSE: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-751-798-8

i Sequence 8, Application US/09751798

j Sequence 8, Application US/09751798

j Patent No. 6225177

GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth; Jager, Elke;

APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;

APPLICANT: Chuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Associated Proteins, Uses Thereof,

TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA

TITLE OF INVENTION: Binding Peptides Derived Therefrom

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

GITTY: New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: 184
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION NUMBER: 08/725,182
PRIOR APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SIN, Eric, Patent Agent REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: 1UD 5466.1
TELECOMMNICATION INFORMATION:
TELECOMMNICATION INFORMATION:
TELEFAX: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
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Matches
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Gaps
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100.0%; Pred. No. 0.69;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.69;
cive 0; Mismatches 0; Indels
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Batent No. 668147

GENERAL INFORMATION:

APPLICANT: Genlan, Matthew J.

APPLICANT: Gran, Ali O.

APPLICANT: Chen, Ison

APPLICANT: Chen, Ison

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

FILE REFERENCE: L0461/7062

CURRENT PAPLICATION NUMBER: US/09/392,714A

CURRENT FILING DATE: 1999-09-09

EARLIER FILING DATE: 1999-09-09

SAFTHER FILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 3.0
ZIP. 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                   COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/751,798
FILING DATE:
                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
APPLICATION NUMBER: 08/725,182
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6525177man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pr.
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Best Local Similarity 100.00
Best Local Similarity 100.00
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Best Local Similarity 100.
The conservative
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TOPOLOGY: linear
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Gaps
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<151> 1998-01-27
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Pred. No. 0.69;
; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Goon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/09849602
Patent No. 6794501
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Stockert, APPLICANT: Stockert, Stockert, TITLE OF INVENTION: Colon Cancer Antigen Panel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: Wolf, Greenfield & Sacks, P.C.
600 Atlantic Avenue
                   NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: L0461/7105(JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: PCT/US98/01445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08791495
Patent No. 5811519
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Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
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SOFTWARE: Patentin version 3.0
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MEDIUM TYPE: Floppy
                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 11; Conserv
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LENGTH: 180
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                                                               SEQ ID NO 9
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                               Sequence 15, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:
APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED FEFTIESS CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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APPLICATION NUMBER: US/09/165,546D FILING DATE: 02-Oct-1998 CLASSIFICATION S30 PRIOR APPLICATION NUMBER: 09/062,422 FILING DATE: APPLICATION NUMBER: 08/937,243 FILING DATE: September 15, 1997 APPLICATION NUMBER: US 08/725,182 FILING DATE: September 15, 1997 APPLICATION NUMBER: US 08/725,182 FILING DATE: COCCODER: J 1996 APPLICATION NUMBER: US 08/725,182 FILING DATE: September 15, 1997 APPLICATION NUMBER: US 08/725,182 FILING DATE: COCCODER: J 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, No. 6723812man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 60; DB 2; Length 180; 100.0%; Pred. No. 0.69;
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APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09341829A Patent No. 6794131
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                           SZQUENCES: 15
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Best Local Similarity 100.
Matches 11; Conservative
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ZIP: 10158
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              US-09-165-546D-15
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Pred. No. 8.6;
0; Mismatches 1; Indels
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Pred. No. 8.6;
0; Mismatches 1; Indels
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L0461/7005
                                                                                                                                                                                                                                                                                                                                         APPLICALL...
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REGISTRATION NUMBER: L0467
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09341829A Patent No. 6794131
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90.9%;
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INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 210 amino acids
TYPE: amino acid
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Best Local Similarity 90.5
Matches 10; Conservative
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52 RASGPRGGAPR 62
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US-09-341-829A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                              USA
                                                                                                           COUNTRY: US
ZIP: 02210
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09341829A

Patent No. 6794131

GENERAL INPORMATION:
APPLICANT: Leth., Bernard
APPLICANT: Leth., Charles
APPLICANT: Bennerd
APPLICANT: Boon-Fallenr, Daniele
APPLICANT: Boon-Fallenr, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE REFERENCE: LO461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 1; Length 180;
Pred. No. 7.5;
0; Mismatches 1; Indels
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APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
CORRESPONDENCE: 14
CORRESPONDENCE ADDRESS:
              FILING DATE:
CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
FELECOMMUNICATION INFORMATION:
TELEFAX: 617-720-3500
TELEFAX: 617
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match , 86.7%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-341-829A-7
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US-08-791-495-5
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Gaps

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Gaps

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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196, 136

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31759
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APPLICANT: SHERWOOD ET AL.
TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Mhinston, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 2;
Pred. No. 93;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Barp, David J.
REGISTRATION NUMBER: 41,401
REFREENCE/DOCKET NUMBER: 2847-46468/DJE
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAIR: Urgon
COUNTRY: United States of America
ZIP: 97204-298
COMPUTER READABLE PORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,329C
PILING DATE: 01/23/97
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/789,329C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One World Trade Center
STREET: 121 S W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
81.8%;
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Best Local Similarity 81.8
Section 9; Conservative
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STRANDEDNESS: single
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US-08-789-329C-10
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Sequence 117, Application US/09344040C

Sequence 117, Application US/09344040C

Patent No. 6548064

GENERAL INFORMATION:

APPLICANT: Tureci, Ozlem

APPLICANT: Ramensee, Hann Georg

APPLICANT: Ramensee, Hann Georg

APPLICANT: Recompace, Act and Georg

APPLICANT: Remensee, Hann Georg

APPLICANT: Remensee, Hann Georg

APPLICANT: Steen Georg

TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene

TITLE OF INVENTION: Gene, and Uses Thereof

FILE REPERENCE: LUD 5556.1

CURRENT APPLICATION NUMBER: US/09/344,040C

CURRENT PILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR PILING DATE: 1999-06-26

NUMBER OF SEQ ID NOS: 132

SEQ ID NO 117

LENGTH. 0
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PREENT NO. 6673350

GENERAL INFORMATION:
APPLICANT: Tureci', Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Bahin, Ugur
APPLICANT: Fureci', Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Fureudschuh, Michael
APPLICANT: Fureudschuh, Michael
APPLICANT: Fureudschuh, Michael
APPLICANT: Prucy Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT PILING DATE: 1094094033,039A
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-26
NUMBER OF FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 131
SOUTWARE PATENTIN Version 3.2
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US-09-252-991A-31759
; Sequence 31759, Application US/09252991A
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Best Local Similarity 100.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RASGPGGGA 9
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1. 1. 14 1

Query Match 76.7%; Score 46; DB 2; Length 143; Best Local Similarity 72.7%; Pred. NO. 36; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 RASGPGGGAPR 11 || |||| || 56 RAGAPGGGGPR 66

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earch completed: March 13, 2006, 19:5

Search completed: March 13, 2006, 19:18:52 Job time : 20.4471 secs

Appliance Applia

Sequence 4, A Sequence 75, Sequence 75, Sequence 75, Sequence 75, Sequence 88, Sequence 76,

Sequence Seq

Sequence 76, Appl Sequence 5, Appli

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Sequence 1404, Application US/10296734

| Publication No. US20040054137A1
| Publication No. US20040054137A1
| GENERAL INFORMATION:
| APPLICANT: Thompson, Scott A
| TITLE OF INVENTION: Synthetic molecules and uses therefor TITLE REFERENCE: Savine 2003.08-04
| CURRENT FILING DATE: 2003.08-04
| PRIOR PILICATION NUMBER: US/10/296,734
| CURRENT FILING DATE: 2000-05-26
| NUMBER OF SEQ ID NOS: 1507
| SOFTWARE: Patentin version 3.2
| LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 60; DB 4; Length 30; Similarity 100.0%; Pred. No. 0.48; 11; Conservative 0; Mismatches 0; Indels
        US-10-447-101-55
US-10-415-641A-52
US-10-295-027-34-1436
US-10-295-027-348
US-10-188-832-141
US-10-146-473-69
US-10-146-473-69
US-10-296-774-834
US-10-467-67-67-15-75
US-10-677-373-7
US-11-067-159-75
US-10-157-031-88
US-10-157-031-88
US-10-157-031-88
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Sequence 202, Application US/10482029
Fublication No. U0220050037445A1
GENERAL INFORMATION:
APPLICANT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REFERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Patentin version 3.1
SEQ ID NO 202
LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: NYSOla segment 4
US-10-296-734-1404
  1 RASGPGGGAPR 11
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US-10-482-029-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
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  TYPE: PRT
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Sequence 1270, Ap
Sequence 7, Appli
Sequence 3, Appli
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5024, Ap
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Sequence 27, Appl
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                                                                                                                                                       (without alignments)
69.096 Million cell updates/sec
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Sequence 502,
Sequence 74,
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(cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/us108_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/us108_PUBCOMB.pep:*
              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-482-029-202
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US-10-023-182-8
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US-10-207-655-71
US-10-205-024-144
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US-10-295-734-832
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US-10-295-734-832
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US-10-295-734-832
US-10-257-023-11
US-10-77-053-11
US-10-657-023-14
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Maximum Match 100%
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GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlam, Matthww;
APPLICANT: Chen, Yao-tseng; Scanlam, Matthww;
APPLICANT: Chen, Yao-tseng; Scanlam, Matthww;
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: G66 Fifth Avenue
CTTY: New York
STATE: New York
CUTY: USA
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Query Match 100.0%; Score 60; DB 5; Length 179; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 11; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
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APPLICATION NUMBER: 08/725,182
FTLING DATE: October 3, 1996
FREISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 1,100 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEPRAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
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Publication No. US20030165834A1
GENERAL INFORMATION. APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
                                                                                                                                                                                                                                                                Sequence 8, Application US/09751798 Patent No. US20020010321A1
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                                                                                               1 RASGPGGGAPR 11
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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer;
House a property of the Company of the Comp
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COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
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OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: CURKNOWN-
APPLICATION NUMBER: 09/062,422
FILING DATE: CURKNOWN-
APPLICATION NUMBER: 09/062,422
FILING DATE: COCCODER 3, 1996
ATTORNEY/AGENT INFORMATION:
                                   APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTON: CoLon Cancer Antigen Panel
FILE REFERENCE: LO461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Stockert, Elisabeth
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.
Matches 11; Conservative
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                   APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: REITORDE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFERENCE: CTLIMM.21CPIC
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT PILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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Sequence 74, Application US/10117937
Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: SIVARD, John, J.L.
APPLICANT: SIVARD, John, J.L.
APPLICANT: LIU, Liping
APPLICANT: US 2010-04-04
FILE REFERENCE: CTLIMM.027A
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/382,211
PRIOR APPLICATION NUMBER: US 60/3837,017
PRIOR APPLICATION NUMBER: US 60/383,210
PRIOR APPLICATION NUMBER: US 60/383,210
PRIOR APPLICATION NUMBER: US 60/383,210
PRIOR FILING DATE: 2001-11-07
PRIOR PRILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SEQ ID NO 74
LENGTH: 180
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Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: Homo sapiens
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US-10-117-937-74
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Sequence 14, Application US/10364614

Publication No. US20030175250A1

GENERAL INFORMATION:
APPLICANT: JAGER, Elke

APPLICANT: Glatic, Sacha

TILLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP
CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR SELING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.2
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Publication No. US20030118592A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-40110.
CURRENT APPLICANTON NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
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                     Best_Local Similarity 100.0%;
Matches 11; Conservative 0
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-207-655-71
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Best Local Similarity
Matches 11; Conserv
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LENGTH: 180
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US-10-026-066-3
Query Match
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APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-01250018
CURRENT PILING DATE: 2002-11-13
FRICH FILING DATE: 2002-11-13
FRICH FILING DATE: 2000-09-15
FRICH FILING DATE: 2001-11-13
FRICH FILING DATE: 2001-11-15
FRICH FILING DATE: 2001-11-21
FRICH FILING DATE: 2001-11-21
FRICH FILING DATE: 2001-11-21
FRICH FILING DATE: 2001-11-21
FRICH FILING DATE: 2002-11-21
FRICH FILING DATE: 2002-11-21
FRICH FILING DATE: 2002-01-06
FRICH FILING DATE: 2002-02-03
FRICH FRICH FILING DATE: 2002-02-03
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Publication No US20040054137A1

GENERAL INFORMATION:
APPLICANT: Thompson, Scott A

APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 832
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                         Sequence 386, Application US/10295027 Publication No. US20030232350Al GENERAL INFORMATION:
                                                                                                                          APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
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                                                                                                                                                                                                                                                                                                                                    Mack, David H.
Murray, Richard
Watson, Susan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserva
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US-10-296-734-832
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APPLICANT:
APPLICANT:
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RESULT 13
US-10-777-053-11
is Sequence 11. Application US/10777053
is Publication No. US20040132088A1
is GENERAL INFORMATION:
is APPLICANT: Sinard, John J. L.
is APPLICANT: Qiu, Zhiyong
is APPLICANT: Qiu, Zhiyong
is APPLICANT: Lei, Xiang-Dong
is TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION WANNERS: US/10/777,053
is CURRENT APPLICATION NUMBER: 10/292,413
is PRIOR PILING DATE: 2002-11-07
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Sequence 139, Application US/10188832

Publication No. US20040076955A1

SEGNERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha

APPLICANT: Ess Bidecefnology, Inc.
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

CURRENT APPLICATION NUMBER: US/10/188,832

CURRENT APPLICATION NUMBER: US 60/302,814

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-08-03

PRIOR PELING DATE: 2001-08-03

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2002-04-12
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                                                                                               ; OTHER INFORMATION: NYNSOla consensus polypeptide
US-10-296-734-832
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0; Mismatches
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Best Local Similarity 100.
Matches 11; Conservative
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TYPE: PRT
ORGANISM: Artificial
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US-10-657-02-74

SQUENCE 74, Application US/10657022

PUBLICATION NO. US20040180354A1

GENERAL INFORMATION:

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

APPLICANT: Liu, Liping

APPLICANT: Liu, Zheng

TITLE OF INVENTION: EPITOPE SEQUENCES

FILE REFERENCE: MANNK. 032A

CURRENT APPLICATION NUMBER: 06/409123

PRIOR APPLICATION NUMBER: 60/409123

PRIOR RILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 610

SOFTWARE: FASTERO FOR WINDOWS Version 4.0

SEQ ID NO 74
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Best Local Similarity 100.
Matches 11; Conservative
                                 1 RASGPGGGAPR 11
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ORGANISM: Homo sapiens
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Gure, Ali, Old, Lloyd, Ritter, Gerd
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IDM
COMPUTER: IDM
CURRENT APPLICATION DATA:
FILING DATE: 02-Jan-2004
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         DB 4; Length 180;
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                                                                                                                                                                                                                                                                  0; Indels
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FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     Query Match 100.0%; Score 60; DB 4
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SEQ ID NO 11
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORCANISM: HOMO Sapien
US-10-777-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, Norman D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 180 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEO ID NO: 15:
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Sequence 28, Appl
Sequence 3295, App
Sequence 3295, Ap
Sequence 20556, A
Sequence 23806, A
Sequence 28, Appl
Sequence 3369, Ap
Sequence 66, Appli
Sequence 66, Appli
Sequence 67, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Appli
                                                                 March 13, 2006, 19:54:06; Search time 7.50588 Seconds (without alignments) 40.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PUSO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/NSO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-623-15-496

US-11-072-51-3295

US-11-096-568A-23806

US-11-096-568A-23806

US-11-096-568A-23806

US-11-072-512-3369

US-11-072-512-3369

US-11-072-512-3369

US-11-097-568A-26217

US-11-096-568A-26217

US-11-096-568A-26333

US-11-096-568A-22333

US-11-096-568A-22333

US-11-096-568A-22333

US-11-096-568A-22333

US-11-096-568A-22333
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                                                                                                                                                                                                  161667 seqs, 27834885 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                               US-09-529-206E-30
60
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Maximum DB seq length: 200000000
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Match Length
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Sequence 28, Application US/11021441

Sequence 28, Application US/20050249748A1

Sequence 28, Application No. US20050249748A1

SERREAL INFORMATION:
APPLICANT: DUCKETY, William S., Jr.
APPLICANT: COCK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/11/021,441

CURRENT PLING DATE: 2004-12-23

PRIOR FILING DATE: 2004-10-06
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                        184, App
164323, A
164323, A
22845, A
22663, A
12071, App
9, Appli
9, Appli
9, Appli
11165, A
11165, A
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22494, A
22493, A
11283, A
24377, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/11155288
Publication No. US20060008468A1
GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUWOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REPERENCE: MANNK. 05.0A
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR APPLICATION NUMBER: 60/580,969
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PREUSE FREE OF WINDOWS Version 4.0
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US-11-103-077-18
US-11-096-568A-14323
US-11-096-568A-14323
US-11-096-568A-22845
US-11-096-568A-22845
US-11-096-568A-22845
US-11-096-568A-2189
US-11-096-568A-988
US-11-096-568A-988
US-11-086-568A-988
US-11-086-568A-1887
US-11-096-568A-10542
US-11-096-568A-10542
US-11-096-568A-1289
US-11-096-568A-1289
US-11-096-568A-1289
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US-11-096-568A-1289
US-11-096-568A-1289
US-11-096-568A-1289
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Best Local Similarity 100.
Matches 11; Conservative
      618
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US-11-155-288-7
    RESULT 2
US-11-021-441-28
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      SEQ ID NO 7
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sequence 22334, A Sequence 22333, A Sequence 27265, A Sequence 22332, A Sequence 8, Appli

Appli

Sequence

Sequence Sequence Sequence

7762, Ap 2722, Ap 58, Appl

Sequence

Sequence 26217, A Sequence 35, Appl Sequence 7762, Ap

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Sequence 20556, Application US/11096568A

Sequence 20556, Application US/11096568A

Publication No. US20060048240A1

GENERAL INPORMATION:
TILLE OF INVENTION:
TILLE OF
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 678;
30;
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80.0%; Pred. No. 29;
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| LOCATION: (1)...(306)
| OTHER INDEMATION: Ceres Seq. ID no. 12383286
| US-11-096-568A-20556
                                                                                                                                APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, MACHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: OYSHIKAMA, TSUTOMU
APPLICANT: OYSHIKAMA, MOTOVOKI
APPLICANT: MASUHO, YASUHIKO
APPLICANT: MASUHO, YASUHIKO
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
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Pred. No.
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Best Local Similarity 80...
8, Conservative
                                                                          WAGAI, KEIICHI
                                           OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 RÁAGPGGGWP 601
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US-11-072-512-3295
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Sequence 496. Application US/10623155

Publication No. US20050261166A1

SERBERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Rettef, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT PILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 60; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-10-01
PRIOR PLING DATE: 2004-08-05
PRIOR PLING DATE: 2004-07-23
PRIOR PLING DATE: 2004-07-23
PRIOR PLING DATE: 2004-07-23
PRIOR PLING DATE: 2004-06-30
PRIOR PRIING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
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US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
; APPLICANT: GUINTAMA, TOMOYASU
; APPLICANT: GUINTAM, TOMOYASU
; APPLICANT: SATO, HIROYUKI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Fusion protein US-11-021-441-28
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-623-155-496
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Pred. No. 88;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OP INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
                PRIOR APPLICATION NUMBER: 60/586,909
PRIOR FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 537
                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Human ceramide kinase
US-11-179-958A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3369, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
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US-11-037-243-66
; Sequence 66, Application US/11037243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ISOGAI, TAKAO
APPLICANT: GUGIYAMA, TOMOYASU
APPLICANT: GUSUKI, TEFSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: STO, HIROYUKI
APPLICANT: ISHII, SHIZIKO
APPLICANT: YAMAMOTO, UUN-ICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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HIO, YURI
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                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-11-072-512-3369
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                       70.0%; Score 42; DB 7; Length 134; 70.0%; Pred. No. 19; Live 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marchi, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Marchi, Martha
APPLICANT: Mang, Elizabeth
APPLICANT: Shamah, Steven M.
ITILE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
ITILE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
ITILE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
ITILE OF INVENTION: METHOD -041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 365
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Publication No. US20060030537A1
GENERAL INFORMATION:
APPLICANT: Charles E.
APPLICANT: Hannun, Yusef A.
APPLICANT: Pettus, Benjamin J.
APPLICANT: Bielawska, Alicia
TILLE OF INVENTION: Ceramide Kinase and Uses Thereof
FILE REFERENCE: 9175-028-999 (MUSC Ref P0401)
CURRENT APPLICATION NUMBER: US/11/179,958A
                                                                                                                                                                                                                         NAME/KEY: misc_feature
i_LOCATION: (1)..(134)
i_LOCATION: (1)..(134)
i_LOSATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
              FILE REFERENCE: 2750-1592PUSZ
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 23806
LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/11108528 Publication No. US20050261189A1 GENERAL INFORMATION:
                                                                                                                                                          TYPE: PRT ORGANISM: Zea mays subsp. mays
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                       Query Match 70.0
Best Local Similarity 70.0
Matches 7; Conservative
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US-11-096-568A-26217
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APPLICANT: He, Fig. 1900

APPLICANT: Halt1, Bradley A. APPLICANT: Halt1, Bradley A. APPLICANT: Wagenar, Melissa M. APPLICANT: Graziani, Edmund APPLICANT: Summers, Mid APPLICANT: Summers, Mid APPLICANT: Summers, Mid APPLICANT: Rulowski, Kerry APPLICANT: Pong, Kevin Mid APPLICANT: Pong, Kevin Polyketide TITLE OF INVENTION: Bolyketide TITLE OF INVENTION: Bolyketide TITLE OF INVENTION: Polyketide CURRENT APPLICATION NUMBER: US 11/143,980

CURRENT APPLICATION NUMBER: US 60/664,483

PRIOR APPLICATION NUMBER: US 60/576,895

PRIOR APPLICATION NUMBER: US 60/576,895

PRIOR FILING DATE: 2004-06-03

NUMBER OF FILING DATE: 2004-06-03

SOFTWARE: Patentin version 3.3

SEQ ID NOS: 72

LENGTH: 280
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                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-26
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR PILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver: 2.1
SERVING BECONTIN VET: 2.1
Hublication No. US20050287546A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: WANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/11143980 Publication No. US20050272133A1 GENERAL INFORMATION:
APPLICANT: He, Min
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 87.5 Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 GPGGGHPR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GPGGGAPR 11
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US-11-143-980-34
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RESULT 12

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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 26217
LENGTH: 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INVENTION:
APPLICANT: Eulenberg, Karsten
APPLICANT: Eulenberg, Martin
APPLICANT: Meise, Martin
APPLICANT: Molitor, Andreas
APPLICANT: Molitor, Andreas
APPLICANT: Steuernagel, Arnd
TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
FILE REFERENCE: 2923-696
CURRENT FILING DATE: 2005-04-12
PRIOR PLILING DATE: 2005-04-12
PRIOR FILING DATE: 2005-10-14
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: EP 02023560.2
PRIOR FILING DATE: 2002-10-22
PRIOR PLILING DATE: 2002-10-24
PRIOR FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.3
SEQ ID NO 35
LENGTH: 974
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Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 4;
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75.0%; Pred. No. 1.9e+02
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)._(558)
LOTTER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217
Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 35, Application US/10531036; Publication No. US20060015951A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 75.0
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-531-036-35
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US-11-087-099-7762
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APPLICANT: Abad, Mark S. et al.
TILE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7762
LENGTH: 1832
TYPE: RRT
GRAMISM: Podospora anserina
US-11-087-099-7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUCIYANA, TAKAO
APPLICANT: GUGIYANA, TOMOYASU
APPLICANT: GUGIYANA, TOMOYASU
APPLICANT: MAKAMATEU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: YUKI
APPLICANT: YUKI
APPLICANT: TSONO, YUKI
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TAMEGHIKA, ICHIRO
APPLICANT: TOSUKA, KROTUNI
APPLICANT: TOSUKA, KROTUNI
APPLICANT: TOSUKA, KROTUNI
APPLICANT: TOSUKA, MOOTOVUKI
APPLICANT: TOSUKA, MOOTOVUKI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: NOGHRANA, TSUNOYUKI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: TOSUKA, MOOTOVUKI
APPLICANT: MAGHARI, KENJI
APPLICANT: WAGHARI, KENJI
APPLICANT: WAGHARI
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Job time : 7.50588 secs
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Publication No. US20060029945A1
GENERAL INFORMATION:
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56 SGPGGGA 62
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